

SEQUENCE LISTING

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<120> Compositions and Methods for the Detection, Diagnosis  
and Therapy of Hematological Malignancies

<130> 014058-014402PC

<140> US 10/501,841  
<141> 2004-07-14

<150> US 10/057,475  
<151> 2002-01-22

<150> WO PCT/US03/02353  
<151> 2003-01-22

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<170> PatentIn Ver. 2.1

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Asp Ser Ile Val Trp Thr Phe Asn Thr Thr Pro Leu Val Thr Ile Gln  
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Pro Glu Gly Gly Thr Ile Ile Val Thr Gln Asn Arg Asn Arg Glu Arg  
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Lys Asn Asp Ser Gly Ile Tyr Tyr Val Gly Ile Tyr Ser Ser Ser Leu  
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 Phe Ile Cys Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser Pro  
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 Ile Leu Ala Arg Lys Leu Cys Glu Gly Ala Ala Asp Asp Pro Asp Ser  
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 His Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala Asn Thr Val Tyr  
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Tyr Pro Arg Lys Asn Leu Phe Leu Val Glu Val Thr Gln Leu Thr Glu  
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Pro Tyr Leu Phe Gln Met Pro Ala Tyr Ala Ser Ser Ser Lys Phe Val  
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His Ser Ser Pro Thr Thr Gln Ile Thr His Arg Pro Arg Val Ser Arg  
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195 200 205  
  
Thr Ala Ser Lys Ile Ser Ala Leu Glu Gly Leu Leu Lys Pro Gln Thr  
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Pro Ser Tyr Asn His His Thr Arg Leu His Arg Gln Arg Ala Leu Asp  
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Tyr Gly Ser Gln Ser Gly Arg Glu Gly Gln Gly Phe His Ile Leu Ile  
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Pro Thr Ile Leu Gly Leu Phe Leu Leu Ala Leu Leu Gly Leu Val Val  
260 265 270

Lys Arg Ala Val Glu Arg Arg Lys Ala Leu Ser Arg Arg Ala Arg Arg  
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Gly Pro Gly Ala Pro Leu Pro Pro Ala Pro Leu Gln Val Ser Glu Ser  
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<223> Description of Artificial Sequence:Ly1452 open  
reading frame His tag fusion

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Ile Asp Gly Ser Pro Arg Leu Leu Asn Thr Asp His Pro Pro Cys Gln  
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Leu Asp Ile Arg Leu Met Arg His Lys Ala Val Trp Ile Asn Pro Gln  
50 55 60  
  
Asp Val Gln Gln Gln Pro Gln Asp Leu Gln Ser Gln Val Pro Ala Ala  
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Gly Asn Ser Gly Thr His Phe Val Thr Asp Ala Ala Ser Pro Ser Gly  
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Pro Ser Pro Ser Cys Leu Gly Asp Ser Leu Ala Glu Thr Thr Leu Ser  
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Glu Asp Thr Thr Asp Ser Val Gly Ser Ala Ser Pro His Gly Ser Ser  
115 120 125  
  
Glu Lys Ser Ser Ser Phe Ser Leu Ser Ser Thr Glu Val His Met Val  
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Arg Pro Gly Tyr Ser His Arg Val Ser Leu Pro Thr Ser Pro Gly Ile  
145 150 155 160  
  
Leu Ala Thr Ser Pro Tyr Pro Glu Thr Asp Ser Ala Phe Phe Glu Pro  
165 170 175  
  
Ser His Leu Thr Ser Ala Ala Asp Glu Gly Ala Val Gln Val Ser Arg  
180 185 190  
  
Arg Thr Ile Ser Ser Asn Ser Phe Ser Pro Glu Val Phe Val Leu Pro  
195 200 205  
  
Val Asp Val Glu Lys Glu Asn Ala His Phe Tyr Val Ala Asp Met Ile  
210 215 220

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 <211> 3604  
 <212> DNA  
 <213> Homo sapiens

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 cagggactc ctatctgtt tgaatggatt cacaccagcc acaagctcgg aaagatggtg 240  
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Leu Asn Thr Asp His Pro Pro Cys Gln Leu Asp Ile Arg Leu Met Arg  
35 40 45

His Lys Ala Val Trp Ile Asn Pro Gln Asp Val Gln Gln Gln Pro Gln  
50 55 60

Asp Leu Gln Ser Gln Val Pro Ala Ala Gly Asn Ser Gly Thr His Phe  
65 70 75 80

Val Thr Asp Ala Ala Ser Pro Ser Gly Pro Ser Pro Ser Cys Leu Gly  
85 90 95

Asp Ser Leu Ala Glu Thr Thr Leu Ser Glu Asp Thr Thr Asp Ser Val  
100 105 110

Gly Ser Ala Ser Pro His Gly Ser Ser Glu Lys Ser Ser Ser Phe Ser  
 115 120 125  
 Leu Ser Ser Thr Glu Val His Met Val Arg Pro Gly Tyr Ser His Arg  
 130 135 140  
 Val Ser Leu Pro Thr Ser Pro Gly Ile Leu Ala Thr Ser Pro Tyr Pro  
 145 150 155 160  
 Glu Thr Asp Ser Ala Phe Phe Glu Pro Ser His Leu Thr Ser Ala Ala  
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 Asp Glu Gly Ala Val Gln Val Ser Arg Arg Thr Ile Ser Ser Asn Ser  
 180 185 190  
 Phe Ser Pro Glu Val Phe Val Leu Pro Val Asp Val Glu Lys Glu Asn  
 195 200 205  
 Ala His Phe Tyr Val Ala Asp Met Ile Ile Ser Ala Met Glu Lys Met  
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 Asp Thr Asn Ile Lys Gln Glu Ser Gly Ser Ser Thr Ser Ser Tyr Ser  
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 Gly Tyr Glu Gly Cys Ala Val Leu Gln Val Ser Pro Val Thr Glu Thr  
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 Arg Thr Tyr His Asp Val Lys Glu Ile Cys Lys Cys Asp Val Asp Glu  
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 325 330 335  
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 340 345 350  
 Cys Trp Ile Leu Ser Val Val Asn Ser Gln Leu Ala Gly Ser Leu Ser  
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 Ala Ala Gly Ser Ile Val Val Asn Glu Glu Cys Val Arg Lys Asp Phe  
 370 375 380  
 Glu Ser Ser Met Asn Val Val Gln Glu Ile Lys Phe Lys Ser Arg Ile  
 385 390 395 400  
 Arg Gly Thr Glu Asp Trp Ala Pro Pro Arg Phe Gln Ile Ile Phe Asn  
 405 410 415  
 Ile His Pro Pro Leu Lys Arg Asp Leu Val Val Ala Ala Gln Asn Phe  
 420 425 430

Phe Cys Ala Gly Cys Gly Thr Pro Val Glu Pro Lys Phe Val Lys Arg  
 435 440 445  
 Leu Arg Tyr Cys Glu Tyr Leu Gly Lys Tyr Phe Cys Asp Cys Cys His  
 450 455 460  
 Ser Tyr Ala Glu Ser Cys Ile Pro Ala Arg Ile Leu Met Met Trp Asp  
 465 470 475 480  
 Phe Lys Lys Tyr Tyr Val Ser Asn Phe Ser Lys Gln Leu Leu Asp Ser  
 485 490 495  
 Ile Trp His Gln Pro Ile Phe Asn Leu Leu Ser Ile Gly Gln Ser Leu  
 500 505 510  
 Tyr Ala Lys Ala Lys Glu Leu Asp Arg Val Lys Glu Ile Gln Glu Gln  
 515 520 525  
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 Ala Leu Lys Glu Phe Glu Gln Val Pro Gly His Leu Thr Asp Glu Leu  
 545 550 555 560  
 His Leu Phe Ser Leu Glu Asp Leu Val Arg Ile Lys Lys Gly Leu Leu  
 565 570 575  
 Ala Pro Leu Leu Lys Asp Ile Leu Lys Ala Ser Leu Ala His Val Ala  
 580 585 590  
 Gly Cys Glu Leu Cys Gln Gly Lys Gly Phe Ile Cys Glu Phe Cys Gln  
 595 600 605  
 Asn Thr Thr Val Ile Phe Pro Phe Gln Thr Ala Thr Cys Arg Arg Cys  
 610 615 620  
 Ser Ala Cys Arg Ala Cys Phe His Lys Gln Cys Phe Gln Ser Ser Glu  
 625 630 635 640  
 Cys Pro Arg Cys Ala Arg Ile Thr Ala Arg Arg Lys Leu Leu Glu Ser  
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 Val Ala Ser Ala Ala Thr  
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<210> 11  
 <211> 2494  
 <212> DNA  
 <213> Homo sapiens

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 gctctccaga cccccagctg gccatgtggt gagttcaggg cccaaatcaa gtatgtaccag 180  
 caatcaggga actccatatct gtttgaatg gattcacacc agccacaagc ctggaaagat 240  
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caagaagtac tacgttcagca atttctccaa acagctgtcgc 1740  
cattttcaatttgctgagca tcggccaaatgc 1800  
agtgaaggaa attcaggagc agcttccatcggatggcttgc 1860  
tgctaacagctgtgtcaagg aaagggttttatttgc 1920  
atcttcccat ttccagacagcaacatgttaga agatgttgc 1980  
aaacagtgtctccaggatctcgatgtcccg 2040  
cttctgaaaaatgtggcctctgc 2100  
ttcaacatgc ttatgataaccgcatttgc 2160  
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gtttcaaaag aatgcagatt ctgtgtttaatctatatttgc 2280  
caaatgttctgtttggctgtatatttgc 2340  
gaatagtttatgttcaactgatgttgc 2400  
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<211> 635
<212> PRT
<213> Homo sapiens
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20 25 30

Leu Asn Thr Asp His Pro Pro Cys Gln Leu Asp Ile Arg Leu Met Arg  
35 40 45

His Lys Ala Val Trp Ile Asn Pro Gln Asp Val Gln Gln Gln Pro Gln  
50 55 60

Asp Leu Gln Ser Gln Val Pro Ala Ala Gly Asn Ser Gly Thr His Phe  
65 70 75 80

Val Thr Asp Ala Ala Ser Pro Ser Gly Pro Ser Pro Ser Cys Leu Gly  
85 90 95

Asp Ser Leu Ala Glu Thr Thr Leu Ser Glu Asp Thr Thr Asp Ser Val  
100 105 110

Gly Ser Ala Ser Pro His Gly Ser Ser Glu Lys Ser Ser Ser Phe Ser  
 115 120 125  
 Leu Ser Ser Thr Glu Val His Met Val Arg Pro Gly Tyr Ser His Arg  
 130 135 140  
 Val Ser Leu Pro Thr Ser Pro Gly Ile Leu Ala Thr Ser Pro Tyr Pro  
 145 150 155 160  
 Glu Thr Asp Ser Ala Phe Phe Glu Pro Ser His Leu Thr Ser Ala Ala  
 165 170 175  
 Asp Glu Gly Ala Val Gln Val Ser Arg Arg Thr Ile Ser Ser Asn Ser  
 180 185 190  
 Phe Ser Pro Glu Val Phe Val Leu Pro Val Asp Val Glu Lys Glu Asn  
 195 200 205  
 Ala His Phe Tyr Val Ala Asp Met Ile Ile Ser Ala Met Glu Lys Met  
 210 215 220  
 Lys Cys Asn Ile Leu Ser Gln Gln Gln Thr Glu Ser Trp Ser Lys Glu  
 225 230 235 240  
 Val Ser Gly Leu Leu Gly Ser Asp Gln Pro Asp Ser Glu Met Thr Phe  
 245 250 255  
 Asp Thr Asn Ile Lys Gln Glu Ser Gly Ser Ser Thr Ser Ser Tyr Ser  
 260 265 270  
 Gly Tyr Glu Gly Cys Ala Val Leu Gln Val Ser Pro Val Thr Glu Thr  
 275 280 285  
 Arg Thr Tyr His Asp Val Lys Glu Ile Cys Lys Cys Asp Val Asp Glu  
 290 295 300  
 Phe Val Ile Leu Glu Leu Gly Asp Phe Asn Asp Ile Thr Glu Thr Cys  
 305 310 315 320  
 Ser Cys Ser Cys Ser Ser Ser Lys Ser Val Thr Tyr Glu Pro Asp Phe  
 325 330 335  
 Asn Ser Ala Glu Leu Leu Ala Lys Glu Leu Tyr Arg Val Phe Gln Lys  
 340 345 350  
 Cys Trp Ile Leu Ser Val Val Asn Ser Gln Leu Ala Gly Ser Leu Ser  
 355 360 365  
 Ala Ala Gly Ser Ile Val Val Asn Glu Glu Cys Val Arg Lys Asp Phe  
 370 375 380  
 Glu Ser Ser Met Asn Val Val Gln Glu Ile Lys Phe Lys Ser Arg Ile  
 385 390 395 400  
 Arg Gly Thr Glu Asp Trp Ala Pro Pro Arg Phe Gln Ile Ile Phe Asn  
 405 410 415  
 Ile His Pro Pro Leu Lys Arg Asp Leu Val Val Ala Ala Gln Asn Phe  
 420 425 430

Phe Cys Ala Gly Cys Gly Thr Pro Val Glu Pro Lys Phe Val Lys Arg  
 435 440 445  
 Leu Arg Tyr Cys Glu Tyr Leu Gly Lys Tyr Phe Cys Asp Cys Cys His  
 450 455 460  
 Ser Tyr Ala Glu Ser Cys Ile Pro Ala Arg Ile Leu Met Met Trp Asp  
 465 470 475 480  
 Phe Lys Lys Tyr Tyr Val Ser Asn Phe Ser Lys Gln Leu Leu Asp Ser  
 485 490 495  
 Ile Trp His Gln Pro Ile Phe Asn Leu Leu Ser Ile Gly Gln Ser Leu  
 500 505 510  
 Tyr Ala Lys Ala Lys Glu Leu Asp Arg Val Lys Glu Ile Gln Glu Gln  
 515 520 525  
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 Cys Val Lys Glu Arg Ala Leu Phe Val Asn Phe Ala Arg Ile Arg Leu  
 545 550 555 560  
 Ser Ser Ser His Phe Arg Gln Gln His Val Glu Asp Val Gln Arg Ala  
 565 570 575  
 Gly Leu Ala Phe Thr Asn Ser Ala Ser Ser Pro Pro Ser Ala Pro Gly  
 580 585 590  
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 595 600 605  
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 <211> 148  
 <212> DNA  
 <213> Homo sapiens

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<210> 14  
 <211> 4094  
 <212> DNA  
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<212> PRT  
<213> Homo sapiens

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Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg  
35 40 45  
  
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu  
50 55 60  
  
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro  
65 70 75 80  
  
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val  
85 90 95  
  
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp  
100 105 110  
  
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys  
115 120 125  
  
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro  
130 135 140  
  
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile  
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His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly  
165 170 175  
  
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu  
180 185 190  
  
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro  
195 200 205  
  
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly  
210 215 220  
  
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe  
225 230 235 240  
  
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys  
245 250 255

Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu  
 260 265 270  
 Glu Ile Phe Cys Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile  
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 Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr  
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 Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu  
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 Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser  
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 Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro  
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 His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg  
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 Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr  
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 Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu  
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 Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile  
 405 410 415  
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 Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu  
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 Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro  
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 Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr  
 465 470 475 480  
 Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly  
 485 490 495  
 Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr  
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 Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro  
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 Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys  
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Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu  
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 Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala  
 595 600 605  
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 Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser  
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 Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val  
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 Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu  
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 Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly  
 675 680 685  
 Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn  
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 His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro  
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 Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys  
 865 870 875 880  
 Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His  
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Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys  
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Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg  
915 920 925

Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly  
930 935 940

Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln  
945 950 955 960

Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val  
965 970 975

Leu Cys Gly Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val  
980 985 990

Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr  
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cagaggccct tccttgagaa ctgtgggaa ggaggccctg ggggttctt ctgttaggcag 180  
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 Ala Val Gly Gln Leu Gly Val Arg Val Phe His Ser Ser Pro Ala Ala  
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 Ser Ser Leu Asp Phe Ile Gly Gly Pro Ala Ile Leu Leu Gly Leu Ile  
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 Ser Leu Ala Thr Asp Asp His Thr Met Tyr Ala Ala Val Lys Val Leu  
 65 70 75 80  
  
 His Ser Val Leu Thr Ser Asn Ala Met Cys Asp Phe Leu Met Gln His  
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 Ile Cys Gly Tyr Gln Ile Met Ala Phe Leu Leu Arg Lys Lys Ala Ser  
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 Leu Leu Asn His Arg Ile Phe Gln Leu Ile Leu Ser Val Ala Gly Thr  
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 Val Glu Leu Gly Phe Arg Ser Ser Ala Ile Thr Asn Thr Gly Val Phe  
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 Gln His Ile Leu Cys Asn Phe Glu Leu Trp Met Asn Thr Ala Asp Asn  
 145 150 155 160  
  
 Leu Glu Leu Ser Leu Phe Ser His Leu Leu Glu Ile Leu Gln Ser Pro  
 165 170 175  
  
 Arg Glu Gly Pro Arg Asn Ala Glu Ala Ala His Gln Ala Gln Leu Ile  
 180 185 190  
  
 Pro Lys Leu Ile Phe Leu Phe Asn Glu Pro Ser Leu Ile Pro Ser Lys  
 195 200 205  
  
 Ile Pro Thr Ile Ile Gly Ile Leu Ala Cys Gln Leu Arg Gly His Phe  
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 Ser Thr Gln Asp Leu Leu Arg Ile Gly Leu Phe Val Val Tyr Thr Leu  
 225 230 235 240  
  
 Lys Pro Ser Ser Val Asn Glu Arg Gln Ile Cys Met Asp Gly Ala Leu  
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Asp Pro Ser Leu Pro Ala Gly Ser Gln Thr Ser Gly Lys Thr Ile Trp  
 260 265 270  
 Leu Arg Asn Gln Leu Leu Glu Met Leu Leu Ser Val Ile Ser Ser Pro  
 275 280 285  
 Gln Leu His Leu Ser Ser Glu Ser Lys Glu Glu Met Phe Leu Lys Leu  
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 Gly Pro Asp Trp Phe Leu Leu Leu Gln Gly His Leu His Ala Ser  
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 Asp Gly Pro Lys Asp Ser Leu Asp Ala Met Leu Gln Trp Leu Leu Gln  
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 Arg His His Gln Glu Glu Val Leu Gln Ala Gly Leu Cys Thr Glu Gly  
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 Trp Arg Ala Pro Glu Phe Leu Gln Thr Leu Ala Ile Ala Ala Phe Pro  
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 545 550 555 560  
 Gln Leu Leu Leu Arg Glu Leu Leu Gly Ala Ser Ser Pro Lys Gln  
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Trp Leu Pro Leu Glu Val Leu Leu Glu Ala Ser Pro Asp His Ala Thr  
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 Ser Gln Gln Lys Arg Asp Phe Gln Ser Glu Val Leu Leu Ser Ala Met  
 595 600 605  
 Glu Leu Phe His Met Thr Ser Gly Gly Asp Ala Ala Met Phe Arg Asp  
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 Gly Met Phe Ser Ala Asp Pro Arg His Ile Leu Leu Phe Ile Leu Glu  
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 His Ile Met Val Val Ile Glu Thr Ala Ser Ser Gln Arg Asp Thr Val  
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Gln Arg Arg Lys Cys Gly Asn Ile Lys Ala Ala Asn Ala Trp Ala Arg  
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Glu Thr Lys Pro Cys Ser Pro Trp Glu Leu Asp Trp Arg Glu Gly Pro  
 965 970 975

Ala Arg Met Arg Lys Arg Ile Lys Arg Leu Ser Pro Leu Glu Ala Leu  
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Ser Ser Gly Arg His Lys Glu Ser Gln Asp Lys Asn Asp His Ile Ser  
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Pro Ala Leu His Glu Ser Leu His Ser Glu Asp Phe Leu Glu Leu Cys  
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Arg Glu Arg Gln Val Ile Leu Gln Glu Leu Leu Asp Lys Glu Lys Val  
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Thr Gln Lys Phe Ser Leu Val Ile Val Gln Gly His Leu Val Ser Glu  
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Gly Val Leu Leu Phe Gly His Gln His Phe Tyr Ile Cys Glu Asn Phe  
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Thr Leu Ser Pro Thr Gly Asp Val Tyr Cys Thr Arg His Cys Leu Ser  
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Asn Ile Ser Asp Pro Phe Ile Phe Asn Leu Cys Ser Lys Asp Arg Ser  
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Thr Asp His Tyr Ser Cys Gln Cys His Ser Tyr Ala Asp Met Arg Glu  
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Leu Arg Gln Ala Arg Phe Leu Leu Gln Asp Ile Ala Leu Glu Ile Phe  
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Phe His Asn Gly Tyr Ser Lys Phe Leu Val Phe Tyr Asn Asn Asp Arg  
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Ser Lys Ala Phe Lys Ser Phe Cys Ser Phe Gln Pro Ser Leu Lys Gly  
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Lys Ala Thr Ser Glu Asp Thr Leu Asn Leu Arg Arg Tyr Pro Gly Ser  
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 Gly Cys Met Gln Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro  
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 1425 1430 1435 1440  
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 Ile Phe His Pro Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile  
 1460 1465 1470  
 Thr Asp Pro Leu Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe  
 1475 1480 1485  
 Gly Gln Val Pro Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr  
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 Ala Ala Gly Lys Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser  
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Pro Ser Gln Val Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser  
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Glu Ser Pro Lys Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr  
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Tyr Gly Ser Asp Lys Ser  
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<212> PRT  
<213> *Homo sapiens*

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 35 40 45

Ser Asp Arg Gly Met Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp  
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Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu  
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Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His  
 85 90 95

Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu  
 100 105 110

Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys Ile Gly  
 115 120 125

Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro  
 130 135 140

Phe Gln Cys Asn Gln Cys Ser Ser Ala Leu Ser Gly Val Gly Gly Ile  
 145 150 155 160

Arg Leu Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys  
 165 170 175

Ile Gly Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu  
 180 185 190

Arg Pro Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly  
 195 200 205

Asn Leu Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys  
 210 215 220

Cys His Leu Cys Asn Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly  
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His Leu Arg Thr His Ser Val Gly Lys Pro His Lys Cys Gly Tyr Cys  
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Gly Arg Ser Tyr Lys Gln Arg Ser Ser Leu Glu Glu His Lys Glu Arg  
 260 265 270

Cys His Asn Tyr Leu Glu Ser Met Gly Leu Pro Gly Met Tyr Pro Val  
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Ile Lys Glu Glu Thr Asn His Asn Glu Met Ala Glu Asp Leu Cys Lys  
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Ile Gly Ala Glu Arg Ser Leu Val Leu Asp Arg Leu Ala Ser Asn Val  
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Ala Lys Arg Lys Ser Ser Met Pro Gln Lys Phe Leu Gly Asp Lys Cys  
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 Val Val Ser Thr Ser Gly Glu Gln Leu Lys Val Tyr Lys Cys Glu His  
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 <211> 350  
 <212> DNA  
 <213> Homo sapiens

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 <212> DNA  
 <213> Homo sapiens

<400> 28

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 <211> 191  
 <212> PRT  
 <213> Homo sapiens

<400> 29

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Thr	Leu	Ile	Trp	Arg	Leu	Phe	Phe	Leu	Ile	Met	Phe	Leu	Thr	Ile	Ile
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Val	Cys	Gly	Met	Val	Ala	Ala	Leu	Ser	Ala	Ile	Arg	Ala	Asn	Cys	His
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Gln	Glu	Pro	Ser	Val	Cys	Leu	Gln	Ala	Ala	Cys	Pro	Glu	Ser	Trp	Ile
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Gly	Phe	Gln	Arg	Lys	Cys	Phe	Tyr	Phe	Ser	Asp	Asp	Thr	Lys	Asn	Trp
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Thr	Ser	Ser	Gln	Arg	Phe	Cys	Asp	Ser	Gln	Asp	Ala	Asp	Leu	Ala	Gln
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Val	Glu	Ser	Phe	Gln	Glu	Leu	Asn	Phe	Leu	Leu	Arg	Tyr	Lys	Gly	Pro
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Ser	Asp	His	Trp	Ile	Gly	Leu	Ser	Arg	Glu	Gln	Gly	Gln	Pro	Trp	Lys
130															140

  

Trp	Ile	Asn	Gly	Thr	Glu	Trp	Thr	Arg	Gln	Phe	Pro	Ile	Leu	Gly	Ala
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Gly	Glu	Cys	Ala	Tyr	Leu	Asn	Asp	Lys	Gly	Ala	Ser	Ser	Ala	Arg	His
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<212> DNA
<213> Homo sapiens

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<211> 2088
<212> DNA
<213> Homo sapiens

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<211> 334  
<212> PRT  
<213> *Homo sapiens*

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 Gly His Arg Leu Thr Asp Arg Leu Gln Val Ala Ile Lys Val Ile Pro  
 50 55 60  
 Arg Asn Arg Val Leu Gly Trp Ser Pro Leu Ser Asp Ser Val Thr Cys  
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 Pro Leu Glu Val Ala Leu Leu Trp Lys Val Gly Ala Gly Gly His  
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 Pro Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Thr Gln Glu Gly Phe  
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 Cys Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu  
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 Pro Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp  
 195 200 205  
 Ile Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu  
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 Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu Arg  
 225 230 235 240  
 Asp Gln Glu Ile Leu Glu Ala Glu Leu His Phe Pro Ala His Val Ser  
 245 250 255  
 Pro Asp Cys Cys Ala Leu Ile Arg Arg Cys Leu Ala Pro Lys Pro Ser  
 260 265 270

Ser Arg Pro Ser Leu Glu Glu Ile Leu Leu Asp Pro Trp Met Gln Thr  
275 280 285

Pro Ala Glu Asp Val Thr Pro Gln Pro Leu Gln Arg Arg Pro Cys Pro  
290 295 300

Phe Gly Leu Val Leu Ala Thr Leu Ser Leu Ala Trp Pro Gly Leu Ala  
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<210> 33

<211> 1215

<212> DNA

<213> Homo sapiens

<400> 33

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<210> 34

<211> 3144

<212> DNA

<213> Homo sapiens

<400> 34

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 <212> PRT  
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 Arg Arg Arg Ala Arg Lys Lys Thr Val Ser Ala Ser Glu Ser Glu Asp  
 180 185 190  
 Arg Leu Val Ala Glu Gln Glu Thr Glu Pro Ser Lys Glu Leu Ser Lys  
 195 200 205  
 Arg Gln Phe Ser Ser Gly Leu Asn Lys Cys Val Ile Leu Ala Leu Val  
 210 215 220  
 Ile Ala Ile Ser Met Gly Phe Gly His Phe Tyr Gly Thr Ile Gln Ile  
 225 230 235 240  
 Gln Lys Arg Gln Gln Leu Val Arg Lys Ile His Glu Asp Glu Leu Asn  
 245 250 255  
 Asp Met Lys Asp Tyr Leu Ser Gln Cys Gln Gln Glu Gln Glu Ser Phe  
 260 265 270  
 Ile Asp Tyr Lys Ser Leu Lys Glu Asn Leu Ala Arg Cys Trp Thr Leu  
 275 280 285  
 Thr Glu Ala Glu Lys Met Ser Phe Glu Thr Gln Lys Thr Asn Leu Ala  
 290 295 300  
 Thr Glu Asn Gln Tyr Leu Arg Val Ser Leu Glu Lys Glu Glu Lys Ala  
 305 310 315 320  
 Leu Ser Ser Leu Gln Glu Glu Leu Asn Lys Leu Arg Glu Gln Ile Arg  
 325 330 335  
 Ile Leu Glu Asp Lys Gly Thr Ser Thr Glu Leu Val Lys Glu Asn Gln  
 340 345 350  
 Lys Leu Lys Gln His Leu Glu Glu Lys Gln Lys Lys His Ser Phe  
 355 360 365  
 Leu Ser Gln Arg Glu Thr Leu Leu Thr Glu Ala Lys Met Leu Lys Arg  
 370 375 380

Glu Leu Glu Arg Glu Arg Leu Val Thr Thr Ala Leu Arg Gly Glu Leu  
 385 390 395 400

Gln Gln Leu Ser Gly Ser Gln Leu His Gly Lys Ser Asp Ser Pro Asn  
 405 410 415

Val Tyr Thr Glu Lys Lys Glu Ile Ala Ile Leu Arg Glu Arg Leu Thr  
 420 425 430

Glu Leu Glu Arg Lys Leu Thr Phe Glu Gln Gln Arg Ser Asp Leu Trp  
 435 440 445

Glu Arg Leu Tyr Val Glu Ala Lys Asp Gln Asn Gly Lys Gln Gly Thr  
 450 455 460

Asp Gly Lys Lys Lys Gly Gly Arg Gly Ser His Arg Ala Lys Asn Lys  
 465 470 475 480

Ser Lys Glu Thr Phe Leu Gly Ser Val Lys Glu Thr Phe Asp Ala Met  
 485 490 495

Lys Asn Ser Thr Lys Glu Phe Val Arg His His Lys Glu Lys Ile Lys  
 500 505 510

Gln Ala Lys Glu Ala Val Lys Glu Asn Leu Lys Lys Phe Ser Asp Ser  
 515 520 525

Val Lys Ser Thr Phe Arg His Phe Lys Asp Thr Thr Lys Asn Ile Phe  
 530 535 540

Asp Glu Lys Gly Asn Lys Arg Phe Gly Ala Thr Lys Glu Ala Ala Glu  
 545 550 555 560

Lys Pro Arg Thr Val Phe Ser Asp Tyr Leu His Pro Gln Tyr Lys Ala  
 565 570 575

Pro Thr Glu Asn His Ser Arg Pro Tyr Tyr Ala Lys Arg Trp Lys Glu  
 580 585 590

Glu Lys Pro Val His Phe Lys Glu Phe Arg Lys Asn Thr Asn Ser Lys  
 595 600 605

Lys Cys Ser Pro Gly His Asp Cys Arg Glu Asn Ser His Ser Phe Arg  
 610 615 620

Lys Ala Cys Ser Gly Val Phe Asp Cys Ala Gln Gln Glu Ser Met Ser  
 625 630 635 640

Leu Phe Asn Thr Val Val Ile Pro Ile Arg Met Asp Glu Phe Arg Gln  
 645 650 655

Ile Ile Gln Arg Tyr Met Leu Lys Glu Leu Asp Thr Phe Cys Arg Trp  
 660 665 670

Asn Glu Leu Asp Gln Phe Ile Asn Lys Phe Phe Leu Asn Gly Val Phe  
 675 680 685

Ile His Asp Gln Lys Leu Phe Thr Asp Phe Val Asn Asp Val Lys Ile  
 690 695 700

Ile Leu Gly Asn Met Lys Glu Tyr Glu Val Asp Asn Asp Gly Val Phe  
705 710 715 720

Glu Lys Leu Asp Glu Tyr Ile Tyr Arg His Phe Phe Gly His Thr Phe  
725 730 735

Ser Pro Pro Tyr Gly Pro Arg Ser Val Tyr Ile Lys Pro Cys His Tyr  
740 745 750

Ser Ser Leu  
755

<210> 36  
<211> 558  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1)..(558)  
<223> n = g, a, c or t

<400> 36  
ccatggatg gctttctga ccattgggg ccaggccagg ccaggccagg cttagggcag 60  
caaggaccag gccaaagggg cagggcctcc tttggagggg ttgagggta catcctcggc 120  
tggtgtttgc atccaggggt ccagcaggat ctcttccagt gagggtcggg aagaaggttt 180  
ggggccagg caccggcgg a tttagggcaca gcaatcttg ggaaaaacatg ggcttggaa 240  
gtggagctca gcttccagaa tctcctggc cctctcaaag ggaatgtccc cacacaccat 300  
gtcatagagg agatgccc gtgaccagac agtggccggg agtgcattgtt actgggtgtcg 360  
agagatccac tctggggggc tgtacaccc t tgtccatca aagtcatgtt agggttcatc 420  
atgaagcagg gcaccagaac caaaatcaat gagtttggca cagccacggc gttaggtctat 480  
caggatgntc tcatccttga tgtcacatg gacaactnca cgggaaatgg cagtgctgga 540  
tggctgccac tactttgg 558

<210> 37  
<211> 86  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MOD\_RES  
<222> (1)..(86)  
<223> Xaa = any amino acid

<400> 37  
Gln Val Val Ala Xaa Ile Gln His Cys His Ser Arg Gly Val Val His  
1 5 10 15

Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Arg Arg Gly Cys  
20 25 30

Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu Pro  
35 40 45

Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp Ile  
50 55 60

Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu Gly  
65 70 75 80

Ile Xaa Leu Tyr Asp Met  
85

<210> 38  
<211> 584  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1)..(584)  
<223> n = g, a, c or t

<400> 38  
aaataatcca ggcaggagaa gagaggaggg cacacttgg aactccctcc ccacaatacg 60  
tgattattta catttagta attggacaat cccggctcag gaggaggtt caagaatctg 120  
caaaagttgg agggagcgcc ccaggagaac aaacagcaag ctttatttcc cctagcccat 180  
cccccaaaaa accatccatc ccatcctagt gtcgtgtggt gtccgggtggt gtccatcttc 240  
cattccttcc caaattatgg aagtaagtt cttctcacca gaataagagc acttgggata 300  
acagagtagg gtcccctcac ccaaaaaaaaaaaaaaa aaaaaaaaaaa gaagccttgg ggttaacaaca 360  
gggcatttacc tccccccagaa taaagaatcc tggctgagg caggttaagca gtttgcacca 420  
atatgggacc ctaggcttagg gggaaagggtc ccttactaa aataaaagct actggggat 480  
tggaaaggaaa gcacccttgc ccaagtaaga gcatatgaac taagtttngt tggnggttagt 540  
aggagggngcc aatgtggggt gacacatcat cagaataaga gtcc 584

<210> 39  
<211> 2052  
<212> DNA  
<213> Homo sapiens

<400> 39  
cgcgcgccgc gaatctcaac gctgcccgt ctgcggcgcc ttccgggcca ccagtttctc 60  
tgcttccac cctggcgccc cccagccctg gtcggccagg tgcgtgtccc cggcggtcca 120  
cgccctgcgg gcttagcggg ttcaatctcg tcaatctcg cagcgccacc tccatgttga 180  
ccaaagctct acaggggcct cccgcgc(ccc cccggacccc cagccgcgg ccaggaggca 240  
agatcggga agcgttcgag gcccggatc gactcggccc ctcctgggt aaaaaaaaaa 300  
ttggcaccgt cttcgccagga caccgcctca cagatcgact ccagggtggcc atcaaagtga 360  
ttccccggaa tcgtgtgctg ggctgggtccc cttgtcaga ctcagtcaca tgcccactcg 420  
aagtgcact gctatggaaa gtgggtgcag gtgggtggca ccctggcggtg atccgcctgc 480  
ttgactgggt tgagacacag gagggtttca tgctggctt ctagccgcct ttgcccgc(ccc 540  
agatctct tgactatatac acagagaagg gcccactggg tgaaggccca agccgctgct 600  
tctttggcca agtagtgcc gccatccagg actgcccattc ccgtggagtt gtccatcg 660  
acatcaagga tgagaacatc ctgatagacc tacgcccgtgg ctgtgcctt ctcattgtt 720  
ttggttctgg tgccctgctt catatgttac cctacactga ctttgatggg acaagggtgt 780  
acagcccccc agagtggatc tctcgacacc agtaccatgc actccggcc actgtctgg 840  
caactggcat cctcccttat gacatgggtt gtggggacat tccctttgag agggaccagg 900  
agattctgga agctgagctc cacttccctt cccatgttcc cccagactgc tggccctaa 960  
tccggccgggtt cctggccccc aaaccttctt cccgaccctc actggaaagag atccctgctgg 1020  
acccttggat gcaaacacca gcccggatg tacccttcaa cccctccaaa ggaggccctg 1080  
ccccttggc ctggccctt cttacccttcaa cctggccctgg cctggccctgg cccccaatgg 1140  
tcagaagaggc catcccatgg ccatgttccaa gggatagatg gacattgtt gacttgggtt 1200  
tacaggttcat taccatgttcat taaagtcag tattactaag gtaaggatt gaggatcagg 1260  
ggttagaaga cataaaaccaa gtctggccag ttcccttccc aatcctacaa aggagccttc 1320  
ctcccagaac ctgtgggtccc tgattctgga gggggaaactt cttgcttctc attttgctaa 1380  
ggaaagtttat ttgggtgaag ttgttcccat tctgagcccc gggactcttta ttctgtatgt 1440  
gtgtcacccttcc acattggcac ctcctactac caccacacaa acttagttca tatgcttta 1500

cttggggcaag	ggtgctttcc	ttccaatacc	ccagtagctt	ttatffffgt	aaaggggaccc	1560
tttccccctag	cctagggtcc	catattgggt	caagctgctt	acctgcctca	gcccccaggatt	1620
ctttatattctg	ggggagggtaa	tgccctgttg	ttaccccaag	gctttttttt	tttttttttt	1680
tgggtgaggg	gaccctactc	tgttatccca	agtgcctta	ttctgggtgag	aagaacctta	1740
cttccataat	ttgggaaggg	atggaaagatg	gacaccacccg	gacaccacca	gacactagga	1800
tgggatggat	ggttttttgg	gggatgggct	aggggaaata	aggcttgctg	tttggttctcc	1860
tggggcgctc	cctccaactt	ttgcagattc	ttgcaacctc	ctcctgagcc	gggattgtcc	1920
aattactaaa	atgtaaaataa	tcacgtattg	tggggagggg	agttccaaagt	gtggccctcc	1980
ctcttcctcct	gcctggattta	ttaaaaaaagc	catgtgtgga	aaccctactat	ttaataaaaag	2040
taatagaatc	ag					2052

<210> 40  
<211> 311  
<212> PRT  
<213> *Homo sapiens*

<400> 40  
 Met Leu Thr Lys Pro Leu Gln Gly Pro Pro Ala Pro Pro Gly Thr Pro  
 1 5 10 15  
 Thr Pro Pro Pro Gly Gly Lys Asp Arg Glu Ala Phe Glu Ala Glu Tyr  
 20 25 30  
 Arg Leu Gly Pro Leu Leu Gly Lys Gly Gly Phe Gly Thr Val Phe Ala  
 35 40 45  
 Gly His Arg Leu Thr Asp Arg Leu Gln Val Ala Ile Lys Val Ile Pro  
 50 55 60  
 Arg Asn Arg Val Leu Gly Trp Ser Pro Leu Ser Asp Ser Val Thr Cys  
 65 70 75 80  
 Pro Leu Glu Val Ala Leu Leu Trp Lys Val Gly Ala Gly Gly His  
 85 90 95  
 Pro Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Thr Gln Glu Gly Phe  
 100 105 110  
 Met Leu Val Leu Glu Arg Pro Leu Pro Ala Gln Asp Leu Phe Asp Tyr  
 115 120 125  
 Ile Thr Glu Lys Gly Pro Leu Gly Glu Gly Pro Ser Arg Cys Phe Phe  
 130 135 140  
 Gly Gln Val Val Ala Ala Ile Gln His Cys His Ser Arg Gly Val Val  
 145 150 155 160  
 His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Arg Arg Gly  
 165 170 175  
 Cys Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu  
 180 185 190  
 Pro Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp  
 195 200 205  
 Ile Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu  
 210 215 220

Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu Arg  
225 230 235 240

Asp Gln Glu Ile Leu Glu Ala Glu Leu His Phe Pro Ala His Val Ser  
245 250 255

Pro Asp Cys Cys Ala Leu Ile Arg Arg Cys Leu Ala Pro Lys Pro Ser  
260 265 270

Ser Arg Pro Ser Leu Glu Glu Ile Leu Leu Asp Pro Trp Met Gln Thr  
275 280 285

Pro Ala Glu Asp Val Pro Leu Asn Pro Ser Lys Gly Gly Pro Ala Pro  
290 295 300

Leu Ala Trp Ser Leu Leu Pro  
305 310

<210> 41

<211> 105

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1)..(105)

<223> n = g, a, c or t

<400> 41

ctggaactgc acntagtccc agctctcctc ggccgcggtc tcctcggggn tggtgccgta 60  
cttttggatg gttttctcta cnacntcccg caagcttccn tccag 105

<210> 42

<211> 1125

<212> DNA

<213> Homo sapiens

<400> 42

gtctccccca ctgtcagcac ctcttctgtg tggtgagtgg accgcttacc ccactagg 60  
aagatgtca gcccaggagag ctgcctcagc ctcataagt acttcctctt cgtttcaac 120  
ctcttcttct tcgtcctcgg cagcctgatc ttctgctcg gcatctggat cctcatcgac 180  
aagaccagct tcgtgcctt tggggcttgc gccttcgtgc ctctgcagat ctggtccaaa 240  
gtcctggcca tctcaggaat cttcaccatg ggcacatgcggc tcctgggttgc tggggggcc 300  
ctcaaggagc tccgctgcctt cctgggccttgc tattttggaa tggctgtgtc cctgtttgcc 360  
acacagatca ccctggaaat cctcatctcc actcagcggg cccagctgga gcgaaagctt 420  
cgggacgtcg tagagaaaac catccaaaag tacggcacca accccggagga gaccgcggcc 480  
gaggagagct gggactatgt gcagttccag ctgcgtgtc gcccgtggca ctacccgcag 540  
gactggttcc aagtctcat cctgagaggt aacgggtcg aggccgaccc cggtccctgc 600  
tcctgtaca acttgcggc gaccaacgac tccacaatcc tagataaggt gatcttgc 660  
cagctcagca ggcttggaca cctggcgcgg tccagacaca gtgcagacat ctgcgtgtc 720  
cctgcagaga gccacatcta ccgcgaggc tgccgcagg gcctccagaa gtggctgcac 780  
aacaacctta ttccatagt gggcatttgc ctgggcgtcg gcctactcga gtcgggttc 840  
atgacgctct cgtatattcct gtgcagaaac ctggaccacg tctacaaccc gtcgtctcga 900  
taccgtttagg ccccgccctc cccaaagtcc cggcccgccc cccgtcacgtg cgctgggcac 960  
ttccctgtcg cctgtaaata tttgtttaat ccccaagttcg cctggagccc tccgccttca 1020  
cattccccctg gggaccacg tggctgcgtg cccctgtcg tgcacccctt cccacgggac 1080  
ctggggcttt cgtccacacg ttcctgtccc catctgtcg cctac 1125

<210> 43  
 <211> 281  
 <212> PRT  
 <213> Homo sapiens

<400> 43  
 Met Ser Ala Gln Glu Ser Cys Leu Ser Leu Ile Lys Tyr Phe Leu Phe  
 1 5 10 15

Val Phe Asn Leu Phe Phe Val Leu Gly Ser Leu Ile Phe Cys Phe  
 20 25 30

Gly Ile Trp Ile Leu Ile Asp Lys Thr Ser Phe Val Ser Phe Val Gly  
 35 40 45

Leu Ala Phe Val Pro Leu Gln Ile Trp Ser Lys Val Leu Ala Ile Ser  
 50 55 60

Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu  
 65 70 75 80

Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu  
 85 90 95

Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg  
 100 105 110

Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln  
 115 120 125

Lys Tyr Gly Thr Asn Pro Glu Glu Thr Ala Ala Glu Glu Ser Trp Asp  
 130 135 140

Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp  
 145 150 155 160

Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg  
 165 170 175

Val Pro Cys Ser Cys Tyr Asn Leu Ser Ala Thr Asn Asp Ser Thr Ile  
 180 185 190

Leu Asp Lys Val Ile Leu Pro Gln Leu Ser Arg Leu Gly His Leu Ala  
 195 200 205

Arg Ser Arg His Ser Ala Asp Ile Cys Ala Val Pro Ala Glu Ser His  
 210 215 220

Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn  
 225 230 235 240

Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu  
 245 250 255

Leu Gly Phe Met Thr Leu Ser Ile Phe Leu Cys Arg Asn Leu Asp His  
 260 265 270

Val Tyr Asn Arg Leu Ala Arg Tyr Arg  
 275 280

<210> 44  
<211> 2915  
<212> DNA  
<213> Homo sapiens

<400> 44  
agccccggcc cgatgcccgc gcgcccagga cgccctccccc cgctgctggc ccggccggcg 60  
gcctctactg cgctgctgct gctgctgctg gccatggcg gcggcgccgc ctggggcgcc 120  
cggggccagg aggcggcgcc ggcggcgccg gacgggcccc ccgcggcaga cggcgaggac 180  
ggacaggacc cgacacagcaa gcacctgtac acggccgaca tggtaacgcga cgggatccag 240  
agcgccgcgc acttcgtcat gttcttcgcg ccctgggtg gacactgcca gcggctgcag 300  
ccgacttggaa atgacactggg agacaaatac aacagcatgg aagatgcca agtctatgtg 360  
gctaaagtgg actgcacggc ccactccgac gtgtgctccg cccagggggt gcgaggatac 420  
cccaccttaa agctttcaaa gccaggccaa gaagctgtga agtaccaggg tcctcgggac 480  
ttccagacac tggaaaactg gatgctgcag acactgaacg aggagccagt gacaccagag 540  
ccggaagtgg aaccggccag tgccccccgag ctcaagcaag ggctgtatga gctctcagca 600  
agcaactttg agctgcacgt tgcacaaggc gaccacttta tcaagttctt cgctccgtgg 660  
tgtggtcaact gcaaagccct ggctccaacc tggagcagc tggctctggg ccttgaacat 720  
tccgaaactg tcaagattgg caaggttgat tgtacacagc actatgaact ctgctccgg 780  
aaccaggttc gtggctatcc cactcttctc tgggtccgag atggaaaaaa ggtggatcag 840  
tacaaggggaa agcgggattt ggagtcaactg aggagtagc tggagtcgca gtcgcagcgc 900  
acagagactg gagcgcacgga gaccgtcaag ccctcagagg ccccggtgct ggcagctgag 960  
cccgaggctg acaagggcac tgggttggca ctcactgaaa ataacttcga tgacaccatt 1020  
gcagaaggaa taacccatca caagttttat gctccatggt gtggcatttg taggactctg 1080  
gctcctactt gggaggaact ctctaaaaag gaattccctg gtctggcggt ggtcaagatc 1140  
gccaagaatg tagtcaactgc tgaacggaaat atctgcagca agtattcggt acgaggctac 1200  
cccacgttat tgctttccg aggagggaaag aaagtcaatg agcacagtgg aggcagagac 1260  
cttgactcgt tacaccgctt tgccctgagc caagcggaaag acgaacttta ggaacacacgt 1320  
tgagggtcac ctctccgtcc cagctccgc accctgcgtt taggagttca gtccccacaga 1380  
ggccactggg ttcccaagtgg tggctgtca gaaagcagaa catactaagc gtgaggtatc 1440  
ttctttgtgt gtgtgtttc caagccaaca cactctacag attctttatt aatgtgtaa 1500  
ctcatggta ctgtgtaaac atttcagtg gcgatatac cccttgacc ttctcttgat 1560  
gaaatttaca tggttccctt tgagactaaa atagcgttga gggaaatgaa attgctggac 1620  
tatttggc tcctgagttt agtgattttg gtggaaagaaa gcacatccaa agcatagtt 1680  
acctgcccac gagttctgga aaggttgct tggcgttgcgta ttgacgttcc tctgatctt 1740  
agtcacagt tgactcaata ctgtgttggg ccgttagcatg gaggcattt aatgcaaaa 1800  
acccacaccc ctggaggata ctttcacggc cgctgctggc gcttctgtt ctgtgaatac 1860  
ttctctcagt gtgaggggtt agccgtatg aaagcagcgt tacttctgac cgtgcctgag 1920  
taagagaatg ctgatccat aactttatgt gtcgataactt gtcaatcag ttactgttca 1980  
ggggatcctt ctgtttctca cgggggtgaaa catgtcttta gttcctcatg ttaacacgaa 2040  
gccagagccc acatgaactg ttggatgtct tccttagaaa gggtaggcattt gggaaattcc 2100  
acgaggctca ttctcagtat ctcattaaact cattgaaaga ttccaggatgtt atttgcacc 2160  
tggggtgaca agaccagaca ggcttccca ggcctggta tccagggagg ctctgcagcc 2220  
ctgctgaagg gcccctaacta gagttctaga gtttctgatt ctgtttctca gtgtccctt 2280  
tagaggctt ctataacttgg tctgcttcaa ggaggtcgac cttctaattgt atgaagaatg 2340  
ggatgcattt gatctcaaga ccaaagacag atgtcagtgg gctgctctgg ccctgggtgt 2400  
cacggctgtg gcagctgtt gatgccagtgt cctcttaactc atgctgtcct tggattttt 2460  
cacctctatc tccctggga ataagcacaat acaggcttaa gctctaagat agataggtgt 2520  
ttgtccctttt accatcgagc tacttcccat aataaccact ttgcattccaa cactcttcac 2580  
ccacctccca tacgcaaggg gatgtggata cttggcccaa agtaactggt ggttaggaatc 2640  
ttagaaacaa gaccacttat actgtctgtc tgaggcagaa gataacagca gcatctcgac 2700  
cagcctctgc cttaaaggaa atctttatata atcacgtatg gttcacagat aattcttttt 2760  
ttaaaaaaaac ccaacctccct agagaagcac aactgtcaag agtcttgcattt acacaacttc 2820  
agctttgcattt caccgagtctt gtattccaag aaaatcaaag tggtaacatt tggttgttta 2880  
caactatgata ctttctaaat aaactccctt tttttt 2915

<210> 45  
<211> 432  
<212> PRT  
<213> Homo sapiens

<400> 45  
 Met Pro Ala Arg Pro Gly Arg Leu Leu Pro Leu Leu Ala Arg Pro Ala  
 1 5 10 15  
 Ala Leu Thr Ala Leu Leu Leu Leu Gly His Gly Gly Gly  
 20 25 30  
 Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala Asp Gly  
 35 40 45  
 Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro His Ser Lys His  
 50 55 60  
 Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile Gln Ser Ala Ala His  
 65 70 75 80  
 Phe Val Met Phe Phe Ala Pro Trp Cys Gly His Cys Gln Arg Leu Gln  
 85 90 95  
 Pro Thr Trp Asn Asp Leu Gly Asp Lys Tyr Asn Ser Met Glu Asp Ala  
 100 105 110  
 Lys Val Tyr Val Ala Lys Val Asp Cys Thr Ala His Ser Asp Val Cys  
 115 120 125  
 Ser Ala Gln Gly Val Arg Gly Tyr Pro Thr Leu Lys Leu Phe Lys Pro  
 130 135 140  
 Gly Gln Glu Ala Val Lys Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu  
 145 150 155 160  
 Glu Asn Trp Met Leu Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu  
 165 170 175  
 Pro Glu Val Glu Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr  
 180 185 190  
 Glu Leu Ser Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His  
 195 200 205  
 Phe Ile Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala  
 210 215 220  
 Pro Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val  
 225 230 235 240  
 Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser Gly  
 245 250 255  
 Asn Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp Gly Lys  
 260 265 270  
 Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser Leu Arg Glu  
 275 280 285  
 Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly Ala Thr Glu Thr  
 290 295 300  
 Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala Glu Pro Glu Ala Asp  
 305 310 315 320

Lys Gly Thr Val Leu Ala Leu Thr Glu Asn Asn Phe Asp Asp Thr Ile  
 325 330 335  
 Ala Glu Gly Ile Thr Phe Ile Lys Phe Tyr Ala Pro Trp Cys Gly His  
 340 345 350  
 Cys Arg Thr Leu Ala Pro Thr Trp Glu Glu Leu Ser Lys Lys Glu Phe  
 355 360 365  
 Pro Gly Leu Ala Gly Val Lys Ile Ala Glu Val Asp Cys Thr Ala Glu  
 370 375 380  
 Arg Asn Ile Cys Ser Lys Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu  
 385 390 395 400  
 Leu Phe Arg Gly Gly Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp  
 405 410 415  
 Leu Asp Ser Leu His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu  
 420 425 430

<210> 46  
 <211> 551  
 <212> DNA  
 <213> Homo sapiens

<400> 46  
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 tggtaact tcattcggtgt cctggttct tacaatgtca cccatctcta cacctgcggc 120  
 accttcgcct tcagccctgc ttgtacacctc attgaacttc aagattccta cctgttgccc 180  
 atctcgagg acaaggtcat ggagggaaaa gccaaagcc ccttgacccc cgctcacaag 240  
 catacggtctg tcttgggtgga tggatgctc tattctggta ctatgaacaa cttcctggc 300  
 agtgagccca tcctgatgctg cacactggga tccctggctg tcctcaagac cgacaacttc 360  
 ctccgctggc tgcattcatga cgcctccctt gtggcagcca tcccttcgac ccaggtcgtc 420  
 tacttcttct tcgaggagac agccagcgag tttgacttct ttgagaggct ccacacatcg 480  
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 accaccattcc t 551

<210> 47  
 <211> 3252  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
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 tcggggggat gtggtaagaa ctgctcaccc agaaagtgcc cgggtgcctg tttccccaga 180  
 cttccctggc gacagtctgt ggctgagcat ggcctccca gcccggcc tggacccttg 240  
 gagcctcctg ggcctttcc tcttccaaact gcttcagctg ctgctgccga cgacgaccgc 300  
 gggggggagggc gggcaggggc ccatgcccag ggtcagatac tatgcagggg atgaacgtag 360  
 ggcacttagc ttcttccacc agaaggccct ccaggatttt gacactctgc tcctgagtgg 420  
 tggatggaaat actctctacg tgggggctcg agaagccatt ctggccctgg atatccagga 480  
 tccagggggtc cccaggctaa agaacatgat accgtggcca gccagtgaca gaaaaaaagag 540  
 tgaatgtgcc tttaagaaga agagcaatga gacacagtgt ttcaacttca tccgtgtcc 600  
 ggtttcttac aatgtcaccc atctctacac ctgcggcacc ttgccttca gcccgtctt 660  
 taccttcatt gaacttcaag attcctacct gttgcccatt tcggaggaca aggtcatgga 720  
 gggaaaaggc caaagccctt ttgaccccgc tcacaagcat acggctgtct tgggtggatgg 780  
 gatgctctat tctggtaacta tgaacaactt cctggcagt gagcccatcc tgatgcgcac 840  
 actgggatcc cagcctgtcc tcaagaccga caacttcctc cgctggctgc atcatgacgc 900

ctccttgtg gcagccatcc ctgcacca ggtcgctac ttcttctcg aggagacagc 960  
 cagcgagttt gacttcttg agaggctcc cacatcgccg gtggctagag tctgcaagaa 1020  
 tgacgtggc ggcggaaaagc tgctgcagaa gaagtggacc acttcctga aggcccagct 1080  
 gctctctgca cccagccgg gcagctgccc ttcaacgtca tccgcccacgc ggtcctgctc 1140  
 cccgcccatt ctccccacagc tccccacatc tacgcagtct tcacctccca gtgggcagg 1200  
 tggcgggacc aggagctctg cggttgc cttctcttc ttggacattt aacgtgtctt 1260  
 taaggggaaa ttcaaagat tgaacaaaga aacttcacgc tggactactt ataggggccc 1320  
 tgagaccaac ccccgccag gcagttgctc agtggggccc tcctctgata aggccctgac 1380  
 cttcatgaag gaccatttcc tgatggatga gcaagtggtg gggacgcccc tgctggtgaa 1440  
 atctggcgtg gagtatacac ggctgcagt ggagacagcc cagggcctt atgggcacag 1500  
 ccatcttgc atgtacactgg gaaccacac aggtcgctc cacaaggctg tggtaagtgg 1560  
 ggacagcagt gtcatctgg tggaaagat tcagctgtc cctgaccctg aacctgttgc 1620  
 caacctgca gctggcccca cccagggtgc agtggggta ggcttctc gaggtgtctg 1680  
 gaggggtgccc cgagccaact gtatgtcta tgagagctgt gtggactgtg tccttgcgg 1740  
 ggaccccccac tggccttggg accctgatc cggaaacctgt tgcctcctgt ctgcccccaa 1800  
 cctgaactcc tggaaagcagg acatggagcg gggaaaccca gagtggcat gtgcactgg 1860  
 ccccatgagc aggagccctt ggcctcagag cccggccaa atcattaaag aagtccctggc 1920  
 tggcccaac tccatctgg agtccccctg ccccccaccc tcaagccttgg cctcttattt 1980  
 ttggagtcat ggcccagcag cagtccttcc agccttcc actgtctaca atggctccct 2040  
 ctgtgtata gtgcaggatg gagttgggg tcttaccag tgctggccaa ctgagaatgg 2100  
 ctttcatac cctgtatct cctactgggt ggacagccag gaccagaccc tggccctgg 2160  
 tcctgaactg gcaggcatcc cccgggagca tggtaaggc cctgtgacca gggtcactgg 2220  
 tggggccgccc ctggctgccc agcagtcttca ctggcccccac ttgtcaactg tcactgtcct 2280  
 ctttgccttta gtgcttctag gagccctcat catcctcgta gctcccccatt tgagagcact 2340  
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 aagcagagag caacacccaa agtctccaa ggaatgcagg acctctgcca gtatgtgg 2460  
 cgctgacaac aactgcctag gcaactgaggt agcttaact ctggcacag gcccggctg 2520  
 cggcggcaggc acctggccat gctggctggg cggcccaagc acaggccctga ctaggatgac 2580  
 agcagcacaa aagaccaccc ttctccctt agaggagctt ctgctactct gcatcactga 2640  
 tgacactca gagggtatg cacagcagtc tgctccctt atgggactcc ctttaccaa 2700  
 gcacatgagc tctctaacag ggtggggct acccccagac ctgctctac actgatattt 2760  
 aagaacctgg agaggatcct tcaaggatgg ccattccagg gaccctccag aaacacagtg 2820  
 ttcaagaga ccctaaaaaa cctgcctgtc ccaggaccc atggtaatga acaccaaaca 2880  
 tctaaacaat catatgctaa catgccactc ctgaaactc cactctgaag ctggcgctt 2940  
 ggacaccaac actcccttct cccagggtca tgcagggtac tgctccctcc tgcttccctt 3000  
 accagtcgtg caccgctgac tcccaggaaat tcttcctgaa agtctgacca cctttcttct 3060  
 tgcttcgtt gggcagact ctatccctt ctggccctggc agaatggcag gggtaatctg 3120  
 agccttcttc actcccttac cctagctgac cccttcaccc tccccctcc cttttccctt 3180  
 gttttggat tcagaaaact gcttgcaga gactgtttat ttttattaa aaatataagg 3240  
 ctatgtatg at 3252

<210> 48  
 <211> 762  
 <212> PRT  
 <213> Homo sapiens

<400> 48  
 Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly Leu  
 1 5 10 15

Phe Leu Phe Gln Leu Leu Gln Leu Leu Pro Thr Thr Thr Ala Gly  
 20 25 30

Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr Ala Gly Asp  
 35 40 45

Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly Leu Gln Asp Phe  
 50 55 60

Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr Leu Tyr Val Gly Ala  
 65 70 75 80  
 Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln Asp Pro Gly Val Pro Arg  
 85 90 95  
 Leu Lys Asn Met Ile Pro Trp Pro Ala Ser Asp Arg Lys Lys Ser Glu  
 100 105 110  
 Cys Ala Phe Lys Lys Ser Asn Glu Thr Gln Cys Phe Asn Phe Ile  
 115 120 125  
 Arg Val Leu Val Ser Tyr Asn Val Thr His Leu Tyr Thr Cys Gly Thr  
 130 135 140  
 Phe Ala Phe Ser Pro Ala Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr  
 145 150 155 160  
 Leu Leu Pro Ile Ser Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser  
 165 170 175  
 Pro Phe Asp Pro Ala His Lys His Thr Ala Val Leu Val Asp Gly Met  
 180 185 190  
 Leu Tyr Ser Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu  
 195 200 205  
 Met Arg Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu  
 210 215 220  
 Arg Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr  
 225 230 235 240  
 Gln Val Val Tyr Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp Phe  
 245 250 255  
 Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys Asn Asp  
 260 265 270  
 Val Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Phe Leu Lys  
 275 280 285  
 Ala Gln Leu Leu Ser Ala Pro Ser Arg Gly Ser Cys Pro Ser Thr Ser  
 290 295 300  
 Ser Ala Thr Arg Ser Cys Ser Pro Pro Ile Leu Pro Gln Leu Pro Thr  
 305 310 315 320  
 Ser Thr Gln Ser Ser Pro Pro Ser Gly Gln Val Gly Gly Thr Arg Ser  
 325 330 335  
 Ser Ala Val Cys Ala Phe Ser Leu Leu Asp Ile Glu Arg Val Phe Lys  
 340 345 350  
 Gly Lys Phe Lys Glu Leu Asn Lys Glu Thr Ser Arg Trp Thr Thr Tyr  
 355 360 365  
 Arg Gly Pro Glu Thr Asn Pro Arg Pro Gly Ser Cys Ser Val Gly Pro  
 370 375 380

Ser Ser Asp Lys Ala Leu Thr Phe Met Lys Asp His Phe Leu Met Asp  
 385 390 395 400  
 Glu Gln Val Val Gly Thr Pro Leu Leu Val Lys Ser Gly Val Glu Tyr  
 405 410 415  
 Thr Arg Leu Ala Val Glu Thr Ala Gln Gly Leu Asp Gly His Ser His  
 420 425 430  
 Leu Val Met Tyr Leu Gly Thr Thr Gly Ser Leu His Lys Ala Val  
 435 440 445  
 Val Ser Gly Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe  
 450 455 460  
 Pro Asp Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly  
 465 470 475 480  
 Ala Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala  
 485 490 495  
 Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg Asp  
 500 505 510  
 Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu Leu Ser  
 515 520 525  
 Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg Gly Asn Pro  
 530 535 540  
 Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser Leu Arg Pro Gln  
 545 550 555 560  
 Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala Val Pro Asn Ser Ile  
 565 570 575  
 Leu Glu Leu Pro Cys Pro His Leu Ser Ala Leu Ala Ser Tyr Tyr Trp  
 580 585 590  
 Ser His Gly Pro Ala Ala Val Pro Glu Ala Ser Ser Thr Val Tyr Asn  
 595 600 605  
 Gly Ser Leu Leu Leu Ile Val Gln Asp Gly Val Gly Gly Leu Tyr Gln  
 610 615 620  
 Cys Trp Ala Thr Glu Asn Gly Phe Ser Tyr Pro Val Ile Ser Tyr Trp  
 625 630 635 640  
 Val Asp Ser Gln Asp Gln Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly  
 645 650 655  
 Ile Pro Arg Glu His Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly  
 660 665 670  
 Ala Ala Leu Ala Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val  
 675 680 685  
 Thr Val Leu Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val  
 690 695 700

Ala Ser Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys  
705 710 715 720

Glu Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His  
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp Ala  
740 745 750

Asp Asn Asn Cys Leu Gly Thr Glu Val Ala  
755 760

<210> 49  
<211> 182  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1)..(182)  
<223> n = g, a, c or t

<400> 49  
accagcagtc ctgcggcacc tacctccgcg tgcgccagcc gccccccagg cccttcctgg 60  
acatggggga gggcaccaag aaccgaatca tcacagccga ggggatcatac ctcctgttct 120  
gcgcgggtggt gcctgggacg ctgctgctgt tnaggaaacg atggcaagaa cganaactcn 180  
gg 182

<210> 50  
<211> 60  
<212> PRT  
<213> Homo sapiens

<220>  
<221> MOD\_RES  
<222> (1)..(60)  
<223> Xaa = any amino acid

<400> 50  
Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro Pro Pro Arg  
1 5 10 15

Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala  
20 25 30

Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu  
35 40 45

Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa  
50 55 60

<210> 51  
<211> 182  
<212> DNA  
<213> Homo sapiens

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<220>
<221> modified_base
<222> (1)..(182)
<223> n = g, a, c or t

<400> 51
accagcagtc ctgcggcacc tacctccgcg tgcgccagcc gccccccagg cccttcctgg 60
acatggggga gggcaccaag aaccgaatca tcacagccga ggggatcatc ctcctgttct 120
gcgcgggtggt gcctgggacg ctgctgtgt tnagggaaacg atggcaagaa cganaactcn 180
gg 182

<210> 52
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (1)..(60)
<223> Xaa = any amino acid

<400> 52
Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro Pro Pro Arg
1 5 10 15

Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala
20 25 30

Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu
35 40 45

Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa
50 55 60

<210> 53
<211> 1107
<212> DNA
<213> Homo sapiens

<400> 53
tgctgcaact caaactaacc aacccactgg gagaagatgc ctgggggtcc aggagtcc 60
caagctctgc ctgccaccat cttcctccct ttcctgtgt ctgctgtcta cctggggcc 120
gggtgccagg ccctgtggat gcacaaggtc ccagcatcat tgatggtgag cttgggggaa 180
gacgcccact tccaaatgccc gcacaatagc agcaacaacg ccaacgtcac ctgggtggc 240
gtcctccatg gcaactacac gtggcccccct gagttctgg gcccggcga ggaccccaat 300
gttacgctga tcatccagaa tgtgaacaag agccatgggg gcatatacgt gtgcggggc 360
caggaggggca acgagtata ccagcagtc tgccgcaccc acctccgcgt ggcgcagcc 420
ccccccaggg cttcctgga catgggggag ggcaccaaga accgaatcat cacagccgag 480
gggatcatcc tcctgttctg cgccgtgggt cctgggacgc tgctgtgtt caggaaacg 540
tggcagaacg agaagctcgg gttggatgcc gggatgaat atgaagatga aaacctttat 600
gaaggcctga acctggacga ctgctccatg tatgaggaca tctccgggg cttccagg 660
acctaccagg atgtgggcag cctcaacata ggagatgtcc agctggagaa gccgtgacac 720
ccctactcct gccaggctgc cccgcctgc tgtgcaccc gctccagtgt ctcagctcac 780
ttccctggga catttcctt tcagcccttc tggggcttc cttagtcata ttccccca 840
gggggtggg aggtaacct cactttctc caggccaggc ctccttggac tcccctgggg 900
gtgtccact cttctccct ctaaactgcc ccacccctta acctaattccc cacgccccgc 960
tgcctttccc aggctccct caccagcgg gtaatgagcc cttaatcgct gcctctaggg 1020
gagctgattt tagcagcctc gtttagtgca cccctccctc cctgatctgt cagggccact 1080
tagtgataat aaattttcc caactgc 1107

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<210> 54  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens

<400> 54  
 Met Pro Gly Gly Pro Gly Val Leu Gln Ala Leu Pro Ala Thr Ile Phe  
 1 5 10 15

Leu Leu Phe Leu Leu Ser Ala Val Tyr Leu Gly Pro Gly Cys Gln Ala  
 20 25 30

Leu Trp Met His Lys Val Pro Ala Ser Leu Met Val Ser Leu Gly Glu  
 35 40 45

Asp Ala His Phe Gln Cys Pro His Asn Ser Ser Asn Asn Ala Asn Val  
 50 55 60

Thr Trp Trp Arg Val Leu His Gly Asn Tyr Thr Trp Pro Pro Glu Phe  
 65 70 75 80

Leu Gly Pro Gly Glu Asp Pro Asn Gly Thr Leu Ile Ile Gln Asn Val  
 85 90 95

Asn Lys Ser His Gly Gly Ile Tyr Val Cys Arg Val Gln Glu Gly Asn  
 100 105 110

Glu Ser Tyr Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro  
 115 120 125

Pro Pro Arg Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile  
 130 135 140

Ile Thr Ala Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly  
 145 150 155 160

Thr Leu Leu Leu Phe Arg Lys Arg Trp Gln Asn Glu Lys Leu Gly Leu  
 165 170 175

Asp Ala Gly Asp Glu Tyr Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn  
 180 185 190

Leu Asp Asp Cys Ser Met Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly  
 195 200 205

Thr Tyr Gln Asp Val Gly Ser Leu Asn Ile Gly Asp Val Gln Leu Glu  
 210 215 220

Lys Pro  
 225

<210> 55  
 <211> 1038  
 <212> DNA  
 <213> Homo sapiens

<400> 55  
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 ccatggggca tcattctgga gtcccctggcc atacttggca tcgtggcac aattctgcta 120  
 ctcttagcat ttctcttcct catgcgaaag atccaagact gcagccagtg gaatgtcctc 180

cccacccagc tcctcttcct cctgagtgtc ctggggctct tcggactcgc ttttgccttc 240  
 atcatcgagc tcaatcaaca aactgccccc gtacgctact ttctcttgg ggttctcttt 300  
 gctctctgtt tctcatgcct cttagctcat gcctccaatc tagtgaagct ggttcggggt 360  
 tgtgtctccct tctcctggac gacaattctg tgcattgcta ttggttgcag tctgttgc当地 420  
 atcattatttgc ccaactgagta tgtgactctc atcatgacca gaggtatgtat gtttgc当地 480  
 atgacacccctt gccagctcaa tgtggacttt gttgtactcc tggtctatgt cctcttc当地 540  
 atggccctca cattttcggt ctccaaagcc accttctgtg gcccgtgtga gaactggaag 600  
 cagcatggaa ggctcatctt tatcaactgtg ctcttctcca tcatcatctg ggtgggtgtgg 660  
 atctccatgc tcttgc当地 gggagg caaccgc当地 ttccagc当地 agccccagtg ggacgacccg 720  
 gtcgtctgca ttgtctggc tcccaacgca tgggtttcc tgcgtgtga categtccc当地 780  
 gagctctgca ttctctacag atcgtgtaga caggagtgc当地 cttaacttcat atggtaactcc cattcagccg 960  
 cccgtcacag cctaccaaca cagcttccaa gtggagaacc aggagctctc cagagccc当地 900  
 gacagtgtatc gagctgagga ggatgttagca ttaacttcat atggtaactcc cattcagccg 1020  
 gagactgttg atcccacaca agagtgttcc atcccacagg ctaaaactaag cccccc当地 1038  
 gatgcaggag gagtataa

<210> 56  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Tyr Lys Asp Cys Ile Glu Ser Thr Gly Asp Tyr Phe Leu Leu Cys  
 1 5 10 15

Asp Ala Glu Gly Pro Trp Gly Ile Ile Leu Glu Ser Leu Ala Ile Leu  
 20 25 30

Gly Ile Val Val Thr Ile Leu Leu Leu Ala Phe Leu Phe Leu Met  
 35 40 45

Arg Lys Ile Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Leu  
 50 55 60

Leu Phe Leu Leu Ser Val Leu Gly Leu Phe Gly Leu Ala Phe Ala Phe  
 65 70 75 80

Ile Ile Glu Leu Asn Gln Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe  
 85 90 95

Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ala His Ala Ser  
 100 105 110

Asn Leu Val Lys Leu Val Arg Gly Cys Val Ser Phe Ser Trp Thr Thr  
 115 120 125

Ile Leu Cys Ile Ala Ile Gly Cys Ser Leu Leu Gln Ile Ile Ile Ala  
 130 135 140

Thr Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Met Met Phe Val Asn  
 145 150 155 160

Met Thr Pro Cys Gln Leu Asn Val Asp Phe Val Val Leu Leu Val Tyr  
 165 170 175

Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe  
 180 185 190

Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ile  
 195 200 205

Thr	Val	Leu	Phe	Ser	Ile	Ile	Ile	Trp	Val	Val	Trp	Ile	Ser	Met	Leu
210															
														220	
Leu	Arg	Gly	Asn	Pro	Gln	Phe	Gln	Arg	Gln	Pro	Gln	Trp	Asp	Asp	Pro
225															240
Val	Val	Cys	Ile	Ala	Leu	Val	Thr	Asn	Ala	Trp	Val	Phe	Leu	Leu	
															255
Tyr	Ile	Val	Pro	Glu	Leu	Cys	Ile	Leu	Tyr	Arg	Ser	Cys	Arg	Gln	Glu
															270
Cys	Pro	Leu	Gln	Gly	Asn	Ala	Cys	Pro	Val	Thr	Ala	Tyr	Gln	His	Ser
275															285
Phe	Gln	Val	Glu	Asn	Gln	Glu	Leu	Ser	Arg	Ala	Arg	Asp	Ser	Asp	Gly
290															300
Ala	Glu	Glu	Asp	Val	Ala	Leu	Thr	Ser	Tyr	Gly	Thr	Pro	Ile	Gln	Pro
305															320
Gln	Thr	Val	Asp	Pro	Thr	Gln	Glu	Cys	Phe	Ile	Pro	Gln	Ala	Lys	Leu
															335
Ser	Pro	Gln	Gln	Asp	Ala	Gly	Gly	Val							
340															345

<210> 57  
 <211> 2457  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
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 cgaatccgag ccgagcggag aggaatccgg ctagagag cggactccag cccgcggacc 120  
 ctgcagccct cgcctgggac agcggcgcgc tggcaggcg cccaagagag catcgagcag 180  
 cgaacccgcg gaagccggcc cgcagccgcg acccgcgac cctgcccgtc tcccgccgccc 240  
 ggtccgggca gcatgaggcg cgccggcgctc tggctctggc tgcgcgcgt ggcgctgagc 300  
 ctgcagccgg ccctgcccga aattgtggct actaatttgc cccctgaaga tcaagatggc 360  
 tctgggatg actctgacaa ctctccggc tcaggtgcag gtgcggcactt agatatcacc 420  
 ttgtcacagc agacccccc cacttggaa gacacgcagc tcctgacggc tattccac 480  
 tctccagaac ccacccggcct ggaggctaca gctgcctcca cctccaccc gccggctgga 540  
 gagggggccca aggagggaga ggctgttagtc ctgcccagaag tggagcctgg cctcaccgccc 600  
 cgggagcagg aggccacccccc ccgacccagg gagaccacac agctcccgac cactcatcag 660  
 gcctcaacga ccacagccac cacggccca gggccgcac cctccaccc ccacagggac 720  
 atgcagccctg gccaccatga gacctaacc cctgcaggac ccagccaaac tgacccatc 780  
 actccccaca cagaggatgg aggtccttct gccaccgaga gggctgtga ggatggagcc 840  
 tccagtacgc tcccacccac agagggtctt gggagcagg acttcaccc ttgaaaccc 900  
 ggggagaata cggctgttagt ggccgtggag cctgacccgc ggaaccagtc cccagtggat 960  
 cagggggccca cggggccctc acagggccctc ctgacccaggaa aagaggtgt gggaggggtc 1020  
 attgccgtat gcctcgtgg gctcatctt gctgtgtgcc tggtggttt catgctgtac 1080  
 cgcacatgaa agaaggacga aggccatc tccttggagg agccaaaca agccaaacggc 1140  
 ggggcctacc agaagccac caaacaggag gaattctatg cctgacccgc gagccatcgc 1200  
 cccccctccgc cctgcacccactc actaggcccc cacttgcctc ttcccttgcag aactgcaggc 1260  
 cctggccctcc cctgcacca ggccacccctc ccagcattcc agcccccctg gtcgctcctg 1320  
 cccacggagt cgtgggtgt gctggagct ccactctgtct tctctgactt ctgcctggag 1380  
 acttagggca ccaggggttt ctgcatagg accttccac cacagccac acctggcattc 1440  
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<210> 58  
 <211> 310  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Met Arg Arg Ala Ala Leu Trp Leu Trp Leu Cys Ala Leu Ala Leu Ser  
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Leu Gln Pro Ala Leu Pro Gln Ile Val Ala Thr Asn Leu Pro Pro Glu  
 20 25 30

Asp Gln Asp Gly Ser Gly Asp Asp Ser Asp Asn Phe Ser Gly Ser Gly  
 35 40 45

Ala Gly Ala Leu Gln Asp Ile Thr Leu Ser Gln Gln Thr Pro Ser Thr  
 50 55 60

Trp Lys Asp Thr Gln Leu Leu Thr Ala Ile Pro Thr Ser Pro Glu Pro  
 65 70 75 80

Thr Gly Leu Glu Ala Thr Ala Ala Ser Thr Ser Thr Leu Pro Ala Gly  
 85 90 95

Glu Gly Pro Lys Glu Gly Glu Ala Val Val Leu Pro Glu Val Glu Pro  
 100 105 110

Gly Leu Thr Ala Arg Glu Gln Glu Ala Thr Pro Arg Pro Arg Glu Thr  
 115 120 125

Thr Gln Leu Pro Thr Thr His Gln Ala Ser Thr Thr Thr Ala Thr Thr  
 130 135 140

Ala Gln Glu Pro Ala Thr Ser His Pro His Arg Asp Met Gln Pro Gly  
 145 150 155 160

His His Glu Thr Ser Thr Pro Ala Gly Pro Ser Gln Ala Asp Leu His  
 165 170 175

Thr Pro His Thr Glu Asp Gly Gly Pro Ser Ala Thr Glu Arg Ala Ala  
 180 185 190

Glu Asp Gly Ala Ser Ser Gln Leu Pro Ala Ala Glu Gly Ser Gly Glu  
 195 200 205

Gln Asp Phe Thr Phe Glu Thr Ser Gly Glu Asn Thr Ala Val Val Ala  
210 215 220

Val Glu Pro Asp Arg Arg Asn Gln Ser Pro Val Asp Gln Gly Ala Thr  
225 230 235 240

Gly Ala Ser Gln Gly Leu Leu Asp Arg Lys Glu Val Leu Gly Gly Val  
245 250 255

Ile Ala Val Gly Leu Val Gly Leu Ile Phe Ala Val Cys Leu Val Gly  
260 265 270

Phe Met Leu Tyr Arg Met Lys Lys Asp Glu Gly Ser Tyr Ser Leu  
275 280 285

Glu Glu Pro Lys Gln Ala Asn Gly Gly Ala Tyr Gln Lys Pro Thr Lys  
290 295 300

Gln Glu Glu Phe Tyr Ala  
305 310

<210> 59

<211> 357

<212> DNA

<213> Homo sapiens

<400> 59

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gtcaactctga cctgcttgct gaatttctcc tgctatgggt atccgatcca attgcagtgg 180  
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tctgtcttca cccggagcga gctcaaggtc tccccacagt ggagtcacca tgggaagatt 300  
tgacacgtgcc agttcagga tgcagatggg aagttccctct ccaatgacac ggtgcag 357

<210> 60

<211> 3260

<212> DNA

<213> Homo sapiens

<400> 60

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gtaaatgggt tttttagcac cctgaaaccc tctacgcctg ggagggggcc tgcgtctgga 180  
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gcacactgaa tatccaccccg gtgcacccca atgacagtgg tcagctgggg ctgaggatgg 420  
agtccaaagac tgagaaaatgg atgaaacgaa tacacccaa tgcgtctgaa aggccctttc 480  
cacctcatat ccagctccct ccagaaattc aagatccc ggaagtcact ctgacctgct 540  
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accagagtgg gaagtactgc tgcaggtct ccaatgacgt gggcccccggaa aggtcgaaag 1020  
aagtgtccct gcaagtgcag tatgccccgg aacccctccac ggttcagatc ctccactcac 1080  
cggtgtggaa gggaaatcaa gtcgagttc tttgcattgtc actggccaaat cctcttccaa 1140

caaattacac gtggtaccac aatgggaaag aatgcaggg aaggacagag gagaaggatcc 1200  
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 ctcccgctc ccactacacc tggtttact ggaataacca aagccccc caccacagcc 1980  
 agaagctgag attggagccg gtgaaggatcc agactcggt tgctactgg tgccagggga 2040  
 ccaacagtgt gggcaaggc cgttcgcctc tcagcacct tactgtctac tatagcccg 2100  
 agaccatcg gaggcgatg gctgtggac tcgggtctg ctcgcctc ctcatcctgg 2160  
 caatctgtgg gctcaagctc cagcgcgtt ggaagaggac acagaggccag caggggcttc 2220  
 aggagaattt cagcgccag agcttcttg tgaggaataa aaaggttaga agggccccc 2280  
 tctctgaagg ccccaactcc ctggatgtt acaatccat gatggaaatg ggcatttagt 2340  
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 cccactcac gaatattatg cccagtttgc gcctctgagg gaaagccag aaaaggacag 3060  
 aaacgaagta gaaaggggca cagtcctggc ctggcttctc ctttggaaatg gaggcattgc 3120  
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 cacttcaaag aaaaaaaaaa 3260

<210> 61  
 <211> 847  
 <212> PRT  
 <213> Homo sapiens

<400> 61  
 Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu  
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Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu  
 20 25 30

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala  
 35 40 45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr  
 50 55 60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr  
 65 70 75 80

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly  
 85 90 95

Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn  
 100 105 110

Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp  
 115 120 125

Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His  
 130 135 140

Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr  
 145 150 155 160

Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp  
 165 170 175

Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser  
 180 185 190

Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro  
 195 200 205

Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala  
 210 215 220

Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His  
 225 230 235 240

Thr Pro Lys Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg  
 245 250 255

Glu Gly Asp Ser Val Thr Met Thr Cys Glu Val Ser Ser Asn Pro  
 260 265 270

Glu Tyr Thr Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys  
 275 280 285

Gln Asn Thr Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser  
 290 295 300

Gly Lys Tyr Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser  
 305 310 315 320

Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val  
 325 330 335

Gln Ile Leu His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu  
 340 345 350

Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His  
 355 360 365

Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro  
 370 375 380

Lys Ile Leu Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn  
 385 390 395 400

Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln  
 405 410 415

Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile  
 420 425 430

Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn  
 435 440 445

Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu  
 450 455 460

Pro Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr  
 465 470 475 480

Thr Ile Ala Cys Ala Arg Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro  
 485 490 495

Val Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys  
 500 505 510

Ile Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln  
 515 520 525

Cys Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu  
 530 535 540

Lys Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser  
 545 550 555 560

Ile Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser  
 565 570 575

Ile Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala  
 580 585 590

Pro Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu  
 595 600 605

Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val  
 610 615 620

Ser His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro His His  
 625 630 635 640

Ser Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala  
 645 650 655

Tyr Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu  
 660 665 670

Ser Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val  
 675 680 685

Ala Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys  
 690 695 700

Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly  
 705 710 715 720

Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys  
 725 730 735

Val Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr  
740 745 750

Asn Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro  
755 760 765

Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln  
770 775 780

Arg Pro Pro Arg Thr Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His  
785 790 795 800

Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu  
805 810 815

Asp Glu Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu  
820 825 830

Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His  
835 840 845

<210> 62

<211> 340

<212> DNA

<213> Homo sapiens

<400> 62

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cacctacaga ccacttcaact tcccctgtcc gcagcgtcacat tatgtcctca taggtggctg 180  
tctggtaat gtccaggccc tcgttaggtgt gatcttcctc catgccagcc ttgctgtcat 240  
ccttgtccag cagcaggaag ataggcacga ttagtgaagag gatgatcagc agcgtctgga 300  
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<210> 63

<211> 79

<212> PRT

<213> Homo sapiens

<400> 63

Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Gln Thr  
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Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Asp  
20 25 30

Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly  
35 40 45

Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg  
50 55 60

Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu  
65 70 75

<210> 64  
 <211> 340  
 <212> DNA  
 <213> Homo sapiens

<400> 64  
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 cacctacaga ccacttcaact tcccctgtcc gcagcgtcac tatgtcctca taggtggctg 180  
 tctggtaat gtccaggccc tcgttaggtgt gatcttctc catgccagcc ttgctgtcat 240  
 ccttgcacag cagcaggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300  
 tcatgtatgat accatccttc accgtgttcc tctgcttcag 340

<210> 65  
 <211> 1226  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
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 gccagatcg aggaccggta ccggaatccc aaaggttagtgc ttggttcgcg gatctggcag 180  
 agccacgtt tcatagccag gaaacggggc ttacacggta aaatgcactg ctacatgaac 240  
 aggcgcctccg gcaatgtgag ctggctctgg aagcaggaga tggacgagaa tccccagcag 300  
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 ggcatggagg aagatcacac ctacgaggcgc ctggacattt accagacagc cacctatgag 660  
 gacatagtga cgctgcggac aggggaagtgc aagtggctgc taggtgagca cccaggccag 720  
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 cctgagaaac caaaaaaaaaaaaaa 1226

<210> 66  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met Val Ala  
 1 5 10 15

Leu Leu Leu Leu Leu Ser Ala Glu Pro Val Pro Ala Ala Arg Ser Glu  
 20 25 30

Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile Trp Gln  
 35 40 45

Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met His  
 50 55 60

Cys	Tyr	Met	Asn	Ser	Ala	Ser	Gly	Asn	Val	Ser	Trp	Leu	Trp	Lys	Gln
65															80
Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg Met															
															95
Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln Gly Ile															
															110
100															
Arg	Phe	Glu	Asp	Asn	Gly	Ile	Tyr	Phe	Cys	Gln	Gln	Lys	Cys	Asn	Asn
	115							120							125
Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met Gly															
	130							135							140
Phe	Ser	Thr	Leu	Ala	Gln	Leu	Lys	Gln	Arg	Asn	Thr	Leu	Lys	Asp	Gly
	145							150				155			160
Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro															
	165							170							175
Ile	Phe	Leu	Leu	Leu	Asp	Lys	Asp	Asp	Ser	Lys	Ala	Gly	Met	Glu	Glu
	180							185							190
Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu															
	195							200							205
Asp	Ile	Val	Thr	Leu	Arg	Thr	Gly	Glu	Val	Lys	Trp	Ser	Val	Gly	Glu
	210							215							220
His	Pro	Gly	Gln	Glu											
	225														

<210>	67														
<211>	449														
<212>	DNA														
<213>	Homo sapiens														
<220>															
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<222>	(16)														
<223>	n = g, a, c or t														
<400>	67														
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cctctcaagt	gttgcattgt	ccctgcctaa	accaagaagg	ctaaacaaag	cccctcctgt	180									
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tagtggagct	cattacaaa	taggcatgcc	tcacacacac	agtccaaagg	caagacactg	300									
gctttgaaat	taggctcatg	atgtgattcc	tattatatgt	acctgatttt	tttaggcccc	360									
aggtatgtgg	accagagtta	atgtcatgac	tcttcaaaga	tatgatgaaa	agttgcctta	420									
gaaatctaga	gatgcatgtt	tatthaatt													449
<210>	68														
<211>	2359														
<212>	DNA														
<213>	Homo sapiens														

<400> 68  
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ttatgctaac ctctgttgc tgatgacatg tcctcagagac tctgatatta aaactcaatc 180  
cttagataac agtagctt atcatggaag taggtagcaa tttggattta gaccattctt 240  
agttatttt ttcttaatga attgatacat gcactttaaa aaatattttt gttatttgg 300  
gaagaaaaac tcagactttt aaaaaagtgt atattgtccc attataatat gtatatggaa 360  
gagtgaaatc tgaacgctgt cttatattaa gcagtagaaat taggtattat cataaaaaagt 420  
cttaatctgt agggaatatg agtttatgtt tatgagtcct gctcagtccc tctttgagag 480  
aattagttga aacccagact ctaaagtctg ctttatattt tggttggattt gaccacttat 540  
ctgcagaagg ttgccttta accccagtggtt ttctaagggtg tggaatttgag tgaccctaat 600  
atttacataaa gagacttgtt tttagtggagc ataaggggagg ggcataagtt acaccgtttt 660  
gtgctgctt agaactgtt tttaaaattt gtcacaaacga gggaaaacaa aataaaattt 720  
gggggcaaaag ggtaggagta tggggggagg ggagagcaaa cctatcgaat atatctttaga 780  
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cacagtccaa aggcaagaca ctggcttgc aattaggctc atgatgtgat tccttattata 1020  
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cactgttttca tctttttctt taaaataca aaagtatccc aactaatcat ttattatggt 2040  
cagctgttt tacatgtccc ctatgtatgg aaatgctatc aacatctgtg atttctaaga 2100  
gtcttaccaa attgttactt taattttctgt gtcctgctga gtgggttttc ttttaaaaata 2160  
ccatttttat caccctgtgg cactgggtgt gttactgcga ttacactgat gattctgagc 2220  
tgtgttctt caagtagctc agtttttgcgtt ttttatattt ggttaacagtt ttgtgtatgt 2280  
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<210> 69  
<211> 240  
<212> DNA  
<213> *Homo sapiens*

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ggtccaattc attatgccaa agggtccgtc taggaggttc ttgttccaag tattgagatt 180
cccgagagaa gtaggtcccc ttagatagaa gcagagttc tcagaggtat ttagcagcag 240
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<210> 70
<211> 980
<212> DNA
<213> Homo sapiens
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<400> 70  
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 tgcttctatc taaggggacc tacttcttc gggaatctca atacttggaa caagaacctc 180  
 ctagacggac ctttggcat aatgaattgg accaactgtg ggttccagga ctagagagcc 240  
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 ttttacatggta tgggagcage ttcaccaacc cctgcaaatg gactctgaag aagacgacaa 600  
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 gctacataacc ttggatagat 980

<210> 71  
 <211> 118  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 71  
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 Ala Ser Leu Arg Arg Thr Pro Ala Ser Pro Ser Asp Ala Ile Gln Arg  
 20 25 30  
  
 Ala Leu Pro Gly Arg Lys Leu Pro Arg Trp Asn Ala Ser Pro Glu Gln  
 35 40 45  
  
 Arg Val Ala Val Pro Cys Gly Gly Leu Thr Gln Trp Leu Asn Thr Gly  
 50 55 60  
  
 Lys Glu Leu Ala Leu Gly Val Arg Thr Ser Glu Thr Cys Arg Leu Gly  
 65 70 75 80  
  
 Ala Val His Gly Trp Glu Gln Leu His Gln Pro Leu Gln Ser Asp Ser  
 85 90 95  
  
 Glu Glu Asp Asp Lys Pro Cys Ser Ser His Thr Arg Lys Leu Thr Gly  
 100 105 110  
  
 Pro Arg Thr Ala Glu Ala  
 115

<210> 72  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
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 <222> (519)  
 <223> n = g, a, c or t

<400> 72  
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tgataaaaat attttaagc cgtaaaagtt atgagatatt ctggtaagc ctgattatca 180  
aagaataccca caaatagctt tggagatcgt gtattgtttg tcactgagtc aaagagatct 240  
gtgggattgt gaggattctt ggggggggg gtgactaatac ctgcacgtcc ctttgtgaag 300  
actccagtaa gtactcgac aacgtacatg tgcttctcc cattgcgtgc tggcttggag 360  
taggtgtccct tggcagaata actggcatcc acagaaaaat agttcctt tccataggat 420  
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ctgcattctgt cccatggaaag aggagtctt cattattttt atggtcattc t 531

<210> 73  
<211> 1956  
<212> DNA  
<213> Homo sapiens

<400> 73  
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ctaactggc aagaataaaat cccaaacaagg ccaggattcc catggcagga gatacccaag 180  
gtgtggtcgg gactgtctt aaggcttgc tcacagcata tgaaatgaaa atcgggtgcaa 240  
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caacagcaag gacatttaat cggaaatcag gtgtgtcaag agctatttttta gaaggtgctg 360  
gacaagctgt ggaaagtgaa tggatgttgc tagctgcaca gcctcacaga gattttataaa 420  
ttacaccagg tggatgttca aagtgcaaaa taataattca tggatgttgc gggaaaagatg 480  
tcaggaaaac ggtcaccagt gttctagaag agtgcatac gaggaaatgtt acatcggtt 540  
cccttccagc catttggaaaca gggaaatggccg gaaaaaaaccc tatcacaatgtt gctgataaca 600  
taatcgatgc tatttgcatac ttcttcatcac aacattccac cccatcatta aaaacagttt 660  
aagttgtcat ttttcaaccc gagctgttca atatatttca cgacagcatg aaaaaaaagag 720  
acctctctgc atcactgaac tttcagttca catttccat gactacatgt aatcttcctg 780  
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cagaatataa taccataaaag gacaagttca cccgaacttgc ttcttcctac gcaatagaga 900  
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gcctgtttaa gcagatgaaa gtttccctt taggtgtccaa aatgttgc aatgttgc 1500  
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ccttattaaag gaaaacttgc caatgttca gctgaaatgttca ctgaatcaca gaatattaaac 1860  
tctgttatgg aacaaatcat aacatgttca acctgttgc atttcaggttca aaaaatgttgc 1920  
gcattgtttaa ctaatattaa aaaatttaccc ccaattt 1956

<210> 74  
<211> 444  
<212> PRT  
<213> Homo sapiens

<400> 74  
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Ser Asn Cys Phe Tyr Phe Gln Ala Phe Leu Asp Glu Phe Thr Asn Trp  
                  20                 25                 30

Ser Arg Ile Asn Pro Asn Lys Ala Arg Ile Pro Met Ala Gly Asp Thr  
                  35                 40                 45

Gln Gly Val Val Gly Thr Val Ser Lys Pro Cys Phe Thr Ala Tyr Glu  
                  50                 55                 60

Met Lys Ile Gly Ala Ile Thr Phe Gln Val Ala Thr Gly Asp Ile Ala  
                  65                 70                 75                 80

Thr Glu Gln Val Asp Val Ile Val Asn Ser Thr Ala Arg Thr Phe Asn  
                  85                 90                 95

Arg Lys Ser Gly Val Ser Arg Ala Ile Leu Glu Gly Ala Gly Gln Ala  
                  100                 105                 110

Val Glu Ser Glu Cys Ala Val Leu Ala Ala Gln Pro His Arg Asp Phe  
                  115                 120                 125

Ile Ile Thr Pro Gly Gly Cys Leu Lys Cys Lys Ile Ile Ile His Val  
                  130                 135                 140

Pro Gly Gly Lys Asp Val Arg Lys Thr Val Thr Ser Val Leu Glu Glu  
                  145                 150                 155                 160

Cys Glu Gln Arg Lys Tyr Thr Ser Val Ser Leu Pro Ala Ile Gly Thr  
                  165                 170                 175

Gly Asn Ala Gly Lys Asn Pro Ile Thr Val Ala Asp Asn Ile Ile Asp  
                  180                 185                 190

Ala Ile Val Asp Phe Ser Ser Gln His Ser Thr Pro Ser Leu Lys Thr  
                  195                 200                 205

Val Lys Val Val Ile Phe Gln Pro Glu Leu Leu Asn Ile Phe Tyr Asp  
                  210                 215                 220

Ser Met Lys Lys Arg Asp Leu Ser Ala Ser Leu Asn Phe Gln Ser Thr  
                  225                 230                 235                 240

Phe Ser Met Thr Thr Cys Asn Leu Pro Glu His Trp Thr Asp Met Asn  
                  245                 250                 255

His Gln Leu Phe Cys Met Val Gln Leu Glu Pro Gly Gln Ser Glu Tyr  
                  260                 265                 270

Asn Thr Ile Lys Asp Lys Phe Thr Arg Thr Cys Ser Ser Tyr Ala Ile  
                  275                 280                 285

Glu Lys Ile Glu Arg Ile Gln Asn Ala Phe Leu Trp Gln Ser Tyr Gln  
                  290                 295                 300

Val Lys Lys Arg Gln Met Asp Ile Lys Asn Asp His Lys Asn Asn Glu  
                  305                 310                 315                 320

Arg Leu Leu Phe His Gly Thr Asp Ala Asp Ser Val Pro Tyr Val Asn  
                  325                 330                 335

Gln His Gly Phe Asn Arg Ser Cys Ala Gly Lys Asn Ala Val Ser Tyr  
340 345 350

Gly Lys Gly Thr Tyr Phe Ala Val Asp Ala Ser Tyr Ser Ala Lys Asp  
355 360 365

Thr Tyr Ser Lys Pro Asp Ser Asn Gly Arg Lys His Met Tyr Val Val  
370 375 380

Arg Val Leu Thr Gly Val Phe Thr Lys Gly Arg Ala Gly Leu Val Thr  
385 390 395 400

Pro Pro Pro Lys Asn Pro His Asn Pro Thr Asp Leu Phe Asp Ser Val  
405 410 415

Thr Asn Asn Thr Arg Ser Pro Lys Leu Phe Val Val Phe Phe Asp Asn  
420 425 430

Gln Ala Tyr Pro Glu Tyr Leu Ile Thr Phe Thr Ala  
435 440

<210> 75

<211> 449

<212> DNA

<213> Homo sapiens

<400> 75

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caggagaaca gagaaaaaac cagcctgtct ccaaactggc ccgtctcagg gactgggggc 180  
cttacccccc agtggaaagat gcagacttta cagcgctgca gtacagtaga gtcagaatgac 240  
tccttcagat agttggatgg gtctctcgat cattcctgat aataacattt tgccatgtt 300  
aagtgttttcc cacctatcat gttaccttct aactactccc ttgggtggat acaggttatta 360  
gccccatttc acaattaaga aattggagct taaaaggatt aaagagttt ttagaggaga 420  
aacagctttt cttacagaa ggatccaa 449

<210> 76

<211> 79

<212> PRT

<213> Homo sapiens

<400> 76

Arg Ser His Leu Thr Leu Leu Tyr Cys Ser Ala Val Lys Ser Ala Ser  
1 5 10 15

Phe Thr Gly Gly Lys Gly Pro Gln Ser Leu Arg Arg Ala Ser Leu Glu  
20 25 30

Thr Gly Trp Phe Phe Leu Cys Ser Pro Glu Ser Pro Ser Asp Glu Lys  
35 40 45

Gly Gly Leu Glu Thr Glu Cys Gln Lys Pro Ile Lys Gly Thr Ala Leu  
50 55 60

His Phe Arg Glu Gly Ala Gly Leu Glu Lys Asn Gln Arg Ser Ser  
65 70 75



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<210> 78
<211> 554
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1)..(554)
<223> n = g, a, c or t

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agntaatttc cattttgaaa attaaaagaa aacagcacag agaagttaaa tgcggtgtag 240
caaagttatg gggctgctt gagggcacta acctcaacag attattccctc ctctccttag 300
aataaccatg aaaatacaaa ttacttagc acattttgc ttttaagta gctggttcat 360
tttctgaatt tcccacattc agagttccag tcattattgt tacatcatgt ttgcagaaaac 420
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tatcaatcta ttat 554

<210> 79
<211> 3243
<212> DNA
<213> Homo sapiens

<400> 79
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ggaccccgcc ccctgccc cagcgcggcc agggaaataca aaagatataa taatgatata 240
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aacaggagat gaacccaaag gaaaaaaga gaagaaagaa gaggaaaaag agcaggagga 1860
ggaagaagac ccatatactt ttgctgagat tgatgacatg gaatatgaca tgatattggc 1920

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agtgttcaa caaaagacag ccagaagaca atctgtatgtat gacaagttcc gtgggtttcc 2100
taagaaacaa gacagagctc ggatagagag tccagccccc tctactctca ggggctgtct 2160
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aaa

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<210> 80  
<211> 755  
<212> PRT  
<213> *Homo sapiens*

<400> 80  
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Val Phe Leu His Val Val Lys Arg Glu Ala Ile Leu Leu Tyr Arg Leu  
20 25 30

Glu Asn Phe Ser Phe Arg His Leu Glu Leu Leu Asn Leu Thr Ser Tyr  
 35 40 45

Lys Cys Lys Leu Leu Ile Leu Ser Asn Ser Leu Leu Arg Asp Leu Thr  
 50 55 60

Pro Lys Lys Cys Gln Phe Leu Glu Lys Ile Leu His Ser Pro Lys Ser  
 65                   70                   75                   80

Val Val Thr Leu Leu Cys Gly Val Lys Ser Ser Asp Gln Leu Tyr Glu  
85 90 95

Leu Leu Asn Ile Ser Gln Ser Arg Trp Glu Ile Ser Thr Glu Gln Glu  
100 105 110

Pro Glu Asp Tyr Ile Ser Val Ile Gln Ser Ile Ile Phe Lys Asp Ser  
 115 120 125

Glu Asp Tyr Phe Glu Val Asn Ile Pro Thr Asp Leu Arg Ala Lys His  
130 135 140

Ser Gly Glu Ile Ser Glu Arg Lys Glu Ile Glu Glu Leu Ser Glu Ala  
145 150 155 160

Ser Arg Asn Thr Ile Pro Leu Ala Val Val Leu Pro Thr Glu Ile Pro  
 165 170 175  
 Cys Glu Asn Pro Gly Glu Ile Phe Ile Ile Leu Arg Asp Glu Val Ile  
 180 185 190  
 Gly Asp Thr Val Glu Val Glu Phe Thr Ser Ser Asn Lys Arg Ile Arg  
 195 200 205  
 Thr Arg Pro Ala Leu Trp Asn Lys Lys Val Trp Cys Met Lys Ala Leu  
 210 215 220  
 Glu Phe Pro Ala Gly Ser Val His Val Asn Val Tyr Cys Asp Gly Ile  
 225 230 235 240  
 Val Lys Ala Thr Thr Lys Ile Lys Tyr Tyr Pro Thr Ala Lys Ala Lys  
 245 250 255  
 Glu Cys Leu Phe Arg Met Ala Asp Ser Gly Glu Ser Leu Cys Gln Asn  
 260 265 270  
 Ser Ile Glu Glu Leu Asp Gly Val Leu Thr Ser Ile Phe Lys His Glu  
 275 280 285  
 Ile Pro Tyr Tyr Glu Phe Gln Ser Leu Gln Thr Glu Ile Cys Ser Gln  
 290 295 300  
 Asn Lys Tyr Thr His Phe Lys Glu Leu Pro Thr Leu Leu His Cys Ala  
 305 310 315 320  
 Ala Lys Phe Gly Leu Lys Asn Leu Ala Ile His Leu Leu Gln Cys Ser  
 325 330 335  
 Gly Ala Thr Trp Ala Ser Lys Met Lys Asn Met Glu Gly Ser Asp Pro  
 340 345 350  
 Ala His Ile Ala Glu Arg His Gly His Lys Glu Leu Lys Lys Ile Phe  
 355 360 365  
 Glu Asp Phe Ser Ile Gln Glu Ile Asp Ile Asn Asn Glu Gln Glu Asn  
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 Asp Tyr Glu Glu Asp Ile Ala Ser Phe Ser Thr Tyr Ile Pro Ser Thr  
 385 390 395 400  
 Gln Asn Pro Ala Phe His His Glu Ser Arg Lys Thr Tyr Gly Gln Ser  
 405 410 415  
 Ala Asp Gly Ala Glu Ala Asn Glu Met Glu Gly Glu Gly Lys Gln Asn  
 420 425 430  
 Gly Ser Gly Met Glu Thr Lys His Ser Pro Leu Glu Val Gly Ser Glu  
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 Ser Ser Glu Asp Gln Tyr Asp Asp Leu Tyr Val Phe Ile Pro Gly Ala  
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 Asp Pro Glu Asn Asn Ser Gln Glu Pro Leu Met Ser Ser Arg Pro Pro  
 465 470 475 480

Leu Pro Pro Pro Arg Pro Val Ala Asn Ala Phe Gln Leu Glu Arg Pro  
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 His Phe Thr Leu Pro Gly Thr Met Val Glu Gly Gln Met Glu Arg Ser  
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 Gln Asn Trp Gly His Pro Gly Val Arg Gln Glu Thr Gly Asp Glu Pro  
                  515                 520                 525  
  
 Lys Gly Glu Lys Glu Lys Glu Glu Glu Lys Glu Gln Glu Glu Glu  
                  530                 535                 540  
  
 Glu Asp Pro Tyr Thr Phe Ala Glu Ile Asp Asp Ser Glu Tyr Asp Met  
                  545                 550                 555                 560  
  
 Ile Leu Ala Asn Leu Ser Ile Lys Lys Lys Thr Gly Ser Arg Ser Phe  
                  565                 570                 575  
  
 Ile Ile Asn Arg Pro Pro Ala Pro Thr Pro Arg Pro Thr Ser Ile Pro  
                  580                 585                 590  
  
 Pro Lys Glu Glu Thr Thr Pro Tyr Ile Ala Gln Val Phe Gln Gln Lys  
                  595                 600                 605  
  
 Thr Ala Arg Arg Gln Ser Asp Asp Asp Lys Phe Arg Gly Leu Pro Lys  
                  610                 615                 620  
  
 Lys Gln Asp Arg Ala Arg Ile Glu Ser Pro Ala Phe Ser Thr Leu Arg  
                  625                 630                 635                 640  
  
 Gly Cys Leu Thr Asp Gly Gln Glu Glu Leu Ile Leu Leu Gln Glu Lys  
                  645                 650                 655  
  
 Val Lys Asn Gly Lys Met Ser Met Asp Glu Ala Leu Glu Lys Phe Lys  
                  660                 665                 670  
  
 His Trp Gln Met Gly Lys Ser Gly Leu Glu Met Ile Gln Gln Glu Lys  
                  675                 680                 685  
  
 Leu Arg Gln Leu Arg Asp Cys Ile Ile Gly Lys Arg Pro Glu Glu Glu  
                  690                 695                 700  
  
 Asn Val Tyr Asn Lys Leu Thr Ile Val His His Pro Gly Gly Lys Glu  
                  705                 710                 715                 720  
  
 Thr Ala His Asn Glu Asn Lys Phe Tyr Asn Val His Phe Ser Asn Lys  
                  725                 730                 735  
  
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                  740                 745                 750  
  
 Lys Asp His  
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 <211> 3195  
 <212> DNA  
 <213> Homo sapiens

<400> 81

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ataatgatat atgaagaaga tgctgagaa tggctctgt acttgacaga agtattttta 240  
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gcttcaagaa acaccatacc actagcgtg gtgttccca ctgaaattcc atgtgagaat 720  
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gtttaaagct aaaaa 3195

<210> 82

<211> 816

<212> PRT

<213> Homo sapiens

<400> 82  
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 35 40 45  
 Cys Gly Pro Ala Pro Pro Gly Asn Thr Lys Asp Ile Ile Met Ile Tyr  
 50 55 60  
 Glu Glu Asp Ala Glu Glu Trp Ala Leu Tyr Leu Thr Glu Val Phe Leu  
 65 70 75 80  
 His Val Val Lys Arg Glu Ala Ile Leu Tyr Arg Leu Glu Asn Phe  
 85 90 95  
 Ser Phe Arg His Leu Glu Leu Leu Asn Leu Thr Ser Tyr Lys Cys Lys  
 100 105 110  
 Leu Leu Ile Leu Ser Asn Ser Leu Leu Arg Asp Leu Thr Pro Lys Lys  
 115 120 125  
 Cys Gln Phe Leu Glu Lys Ile Leu His Ser Pro Lys Ser Val Val Thr  
 130 135 140  
 Leu Leu Cys Gly Val Lys Ser Ser Asp Gln Leu Tyr Glu Leu Leu Asn  
 145 150 155 160  
 Ile Ser Gln Ser Arg Trp Glu Ile Ser Thr Glu Gln Glu Pro Glu Asp  
 165 170 175  
 Tyr Ile Ser Val Ile Gln Ser Ile Ile Phe Lys Asp Ser Glu Asp Tyr  
 180 185 190  
 Phe Glu Val Asn Ile Pro Thr Asp Leu Arg Ala Lys His Ser Gly Glu  
 195 200 205  
 Ile Ser Glu Arg Lys Glu Ile Glu Glu Leu Ser Glu Ala Ser Arg Asn  
 210 215 220  
 Thr Ile Pro Leu Ala Val Val Leu Pro Thr Glu Ile Pro Cys Glu Asn  
 225 230 235 240  
 Pro Gly Glu Ile Phe Ile Ile Leu Arg Asp Glu Val Ile Gly Asp Thr  
 245 250 255  
 Val Glu Val Glu Phe Thr Ser Ser Asn Lys Arg Ile Arg Thr Arg Pro  
 260 265 270  
 Ala Leu Trp Asn Lys Lys Val Trp Cys Met Lys Ala Leu Glu Phe Pro  
 275 280 285  
 Ala Gly Ser Val His Val Asn Val Tyr Cys Asp Gly Ile Val Lys Ala  
 290 295 300  
 Thr Thr Lys Ile Lys Tyr Tyr Pro Thr Ala Lys Ala Lys Glu Cys Leu  
 305 310 315 320

Phe Arg Met Ala Asp Ser Gly Glu Ser Leu Cys Gln Asn Ser Ile Glu  
 325 330 335  
 Glu Leu Asp Gly Val Leu Thr Ser Ile Phe Lys His Glu Ile Pro Tyr  
 340 345 350  
 Tyr Glu Phe Gln Ser Leu Gln Thr Glu Ile Cys Ser Gln Asn Lys Tyr  
 355 360 365  
 Thr His Phe Lys Glu Leu Pro Thr Leu Leu His Cys Ala Ala Lys Phe  
 370 375 380  
 Gly Leu Lys Asn Leu Ala Ile His Leu Leu Gln Cys Ser Gly Ala Thr  
 385 390 395 400  
 Trp Ala Ser Lys Met Lys Asn Met Glu Gly Ser Asp Pro Ala His Ile  
 405 410 415  
 Ala Glu Arg His Gly His Lys Glu Leu Lys Lys Ile Phe Glu Asp Phe  
 420 425 430  
 Ser Ile Gln Glu Ile Asp Ile Asn Asn Glu Gln Glu Asn Asp Tyr Glu  
 435 440 445  
 Glu Asp Ile Ala Ser Phe Ser Thr Tyr Ile Pro Ser Thr Gln Asn Pro  
 450 455 460  
 Ala Phe His His Glu Ser Arg Lys Thr Tyr Gly Gln Ser Ala Asp Gly  
 465 470 475 480  
 Ala Glu Ala Asn Glu Met Glu Gly Glu Gly Lys Gln Asn Gly Ser Gly  
 485 490 495  
 Met Glu Thr Lys His Ser Pro Leu Glu Val Gly Ser Glu Ser Ser Glu  
 500 505 510  
 Asp Gln Tyr Asp Asp Leu Tyr Val Phe Ile Pro Gly Ala Asp Pro Glu  
 515 520 525  
 Asn Asn Ser Gln Glu Pro Leu Met Ser Ser Arg Pro Pro Leu Pro Pro  
 530 535 540  
 Pro Arg Pro Val Ala Asn Ala Phe Gln Leu Glu Arg Pro His Phe Thr  
 545 550 555 560  
 Leu Pro Gly Thr Met Val Glu Gly Gln Met Glu Arg Ser Gln Asn Trp  
 565 570 575  
 Gly His Pro Gly Val Arg Gln Glu Thr Gly Asp Glu Pro Lys Gly Glu  
 580 585 590  
 Lys Glu Lys Lys Glu Glu Glu Lys Glu Gln Glu Glu Glu Asp Pro  
 595 600 605  
 Tyr Thr Phe Ala Glu Ile Asp Asp Ser Glu Tyr Asp Met Ile Leu Ala  
 610 615 620  
 Asn Leu Ser Ile Lys Lys Lys Thr Gly Ser Arg Ser Phe Ile Ile Asn  
 625 630 635 640

Arg	Pro	Pro	Ala	Pro	Thr	Pro	Arg	Pro	Thr	Ser	Ile	Pro	Pro	Lys	Glu
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Glu	Thr	Thr	Pro	Tyr	Ile	Ala	Gln	Val	Phe	Gln	Gln	Lys	Thr	Ala	Arg
660													670		
Arg	Gln	Ser	Asp	Asp	Asp	Lys	Phe	Arg	Gly	Leu	Pro	Lys	Lys	Gln	Asp
675													685		
Arg	Ala	Arg	Ile	Glu	Ser	Pro	Ala	Phe	Ser	Thr	Leu	Arg	Gly	Cys	Leu
690													700		
Thr	Asp	Gly	Gln	Glu	Glu	Leu	Ile	Leu	Leu	Gln	Glu	Lys	Val	Lys	Asn
705													720		
Gly	Lys	Met	Ser	Met	Asp	Glu	Ala	Leu	Glu	Lys	Phe	Lys	His	Trp	Gln
725													735		
Met	Gly	Lys	Ser	Gly	Leu	Glu	Met	Ile	Gln	Gln	Glu	Lys	Leu	Arg	Gln
740													750		
Leu	Arg	Asp	Cys	Ile	Ile	Gly	Lys	Arg	Pro	Glu	Glu	Glu	Asn	Val	Tyr
755													765		
Asn	Lys	Leu	Thr	Ile	Val	His	His	Pro	Gly	Gly	Lys	Glu	Thr	Ala	His
770													780		
Asn	Glu	Asn	Lys	Phe	Tyr	Asn	Val	His	Phe	Ser	Asn	Lys	Leu	Pro	Ala
785													800		
Arg	Pro	Gln	Val	Glu	Lys	Glu	Phe	Gly	Phe	Cys	Cys	Lys	Lys	Asp	His
805													815		

<210> 83  
 <211> 3544  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 gatc 3544

<210> 84  
 <211> 770  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 20 25 30

Phe Leu His Val Val Lys Arg Glu Ala Ile Leu Leu Tyr Arg Leu Glu  
 35 40 45

Asn Phe Ser Phe Arg His Leu Glu Leu Leu Asn Leu Thr Ser Tyr Lys  
 50 55 60

Cys Lys Leu Leu Ile Leu Ser Asn Ser Leu Leu Arg Asp Leu Thr Pro  
 65 70 75 80

Lys Lys Cys Gln Phe Leu Glu Lys Ile Leu His Ser Pro Lys Ser Val  
 85 90 95  
 Val Thr Leu Leu Cys Gly Val Lys Ser Ser Asp Gln Leu Tyr Glu Leu  
 100 105 110  
 Leu Asn Ile Ser Gln Ser Arg Trp Glu Ile Ser Thr Glu Gln Glu Pro  
 115 120 125  
 Glu Asp Tyr Ile Ser Val Ile Gln Ser Ile Ile Phe Lys Asp Ser Glu  
 130 135 140  
 Asp Tyr Phe Glu Val Asn Ile Pro Thr Asp Leu Arg Ala Lys His Ser  
 145 150 155 160  
 Gly Glu Ile Ser Glu Arg Lys Glu Ile Glu Glu Leu Ser Glu Ala Ser  
 165 170 175  
 Arg Asn Thr Ile Pro Leu Ala Val Val Leu Pro Thr Glu Ile Pro Cys  
 180 185 190  
 Glu Asp Pro Gly Glu Ile Phe Ile Ile Leu Arg Asp Glu Val Ile Gly  
 195 200 205  
 Asp Thr Val Glu Val Glu Phe Thr Ser Ser Asn Lys Arg Ile Arg Thr  
 210 215 220  
 Arg Pro Ala Leu Trp Asn Lys Lys Val Trp Cys Met Lys Ala Leu Glu  
 225 230 235 240  
 Phe Pro Ala Gly Ser Val His Val Asn Val Tyr Cys Asp Gly Ile Val  
 245 250 255  
 Lys Ala Thr Thr Lys Ile Lys Tyr Tyr Pro Thr Ala Lys Ala Lys Glu  
 260 265 270  
 Cys Leu Phe Arg Met Ala Asp Ser Gly Glu Ser Leu Cys Gln Asn Ser  
 275 280 285  
 Ile Glu Glu Leu Asp Gly Val Leu Thr Ser Ile Phe Lys His Glu Ile  
 290 295 300  
 Pro Tyr Tyr Glu Phe Gln Ser Leu Gln Thr Glu Ile Cys Ser Gln Asn  
 305 310 315 320  
 Lys Tyr Thr His Phe Lys Glu Leu Pro Thr Leu Leu His Cys Ala Ala  
 325 330 335  
 Lys Phe Gly Leu Lys Asn Leu Ala Ile His Leu Leu Gln Cys Ser Gly  
 340 345 350  
 Ala Thr Trp Ala Ser Lys Met Lys Asn Met Glu Gly Ser Asp Pro Thr  
 355 360 365  
 His Ile Ala Glu Arg His Gly His Lys Glu Leu Lys Lys Ile Phe Glu  
 370 375 380  
 Asp Phe Ser Ile Gln Glu Ile Asp Ile Asn Asn Glu Gln Glu Asn Asp  
 385 390 395 400

Tyr Glu Glu Asp Ile Ala Ser Phe Ser Thr Tyr Ile Pro Ser Thr Gln  
 405 410 415  
 Asn Pro Ala Phe His His Glu Ser Arg Lys Thr Tyr Gly Gln Ser Ala  
 420 425 430  
 Asp Gly Ala Glu Ala Asn Glu Met Glu Gly Glu Gly Lys Gln Asn Gly  
 435 440 445  
 Ser Gly Met Glu Thr Lys His Ser Pro Leu Glu Val Gly Ser Glu Ser  
 450 455 460  
 Ser Glu Asp Gln Tyr Asp Asp Leu Tyr Val Phe Ile Pro Gly Ala Asp  
 465 470 475 480  
 Pro Glu Asn Asn Ser Gln Glu Pro Leu Met Ser Ser Arg Pro Pro Leu  
 485 490 495  
 Pro Pro Pro Arg Pro Val Ala Asn Ala Phe Gln Leu Glu Arg Pro His  
 500 505 510  
 Phe Thr Leu Pro Gly Thr Met Val Glu Gly Gln Met Glu Arg Ser Gln  
 515 520 525  
 Asn Trp Gly His Pro Gly Val Arg Gln Glu Thr Gly Asp Glu Pro Lys  
 530 535 540  
 Gly Glu Lys Glu Lys Lys Glu Glu Glu Lys Glu Gln Glu Glu Glu Glu  
 545 550 555 560  
 Asp Pro Tyr Thr Phe Ala Glu Ile Asp Asp Ser Glu Tyr Asp Met Ile  
 565 570 575  
 Leu Ala Asn Leu Ser Ile Lys Lys Thr Gly Ser Arg Ser Phe Ile  
 580 585 590  
 Ile Asn Arg Pro Pro Ala Pro Thr Pro Arg Pro Thr Ser Ile Pro Pro  
 595 600 605  
 Lys Glu Glu Thr Thr Pro Tyr Ile Ala Gln Val Phe Gln Gln Lys Thr  
 610 615 620  
 Ala Arg Arg Gln Ser Asp Asp Asp Lys Phe Arg Gly Leu Pro Lys Lys  
 625 630 635 640  
 Gln Asp Arg Ala Arg Ile Glu Ser Pro Ala Phe Ser Thr Leu Arg Gly  
 645 650 655  
 Cys Leu Thr Asp Gly Gln Glu Glu Leu Ile Leu Leu Gln Glu Lys Val  
 660 665 670  
 Lys Asn Gly Lys Met Ser Met Asp Glu Ala Leu Glu Lys Phe Lys His  
 675 680 685  
 Trp Gln Met Gly Lys Ser Gly Leu Glu Met Ile Gln Gln Glu Lys Leu  
 690 695 700  
 Arg Gln Leu Arg Asp Cys Ile Ile Gly Lys Arg Pro Glu Glu Glu Asn  
 705 710 715 720

Val Tyr Asn Lys Leu Thr Ile Val His His Pro Gly Gly Lys Glu Thr  
725 730 735

Ala His Asn Glu Asn Lys Phe Tyr Asn Val His Phe Ser Asn Lys Leu  
740 745 750

Pro Ala Arg Pro Gln Val Glu Lys Glu Phe Gly Phe Cys Cys Lys Lys  
755 760 765

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 <211> 313  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(313)  
 <223> n = g, a, c or t

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 tataaaactat taggttgggt caaaaactaat tgggtttttt gccattgaaa tggcattgaa 180  
 ataaaagtgt aaagaaaatct ataccagatg tagtaacagt gtttggttc tgggaggtt 240  
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 atgaatctgt ntt 313

<210> 99  
 <211> 317  
 <212> DNA  
 <213> Homo sapiens

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 tgggctgaag gcgaaatttgc agtccatggc tgaggagaag aggaacgag aggaagagga 180

gaaggcacag caggtggcca ggaggcaaca ggagcgaaag gctgtacaa agaggagccc	240
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gaaaatctcc tcagagg	317

<210> 100  
<211> 1968  
<212> DNA  
<213> Homo sapiens

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cagagagatt atgccaaggc ctttgggtgc cagatggaa tccagaagga cccagtggt 660  
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ccagtttgtt taccgggaa agtacgtcta gattgtgtgg ttgcctcat tggctattt 1860  
gcccaacttcc ttccctgaa gaaatatctg tgaaccttct ttctgttcag tcctaaaatt 1920  
cgaaataaaag tgagactatg gttcacctgt aaaaaaaaaa aaggaatt 1968

<210> 101  
<211> 486  
<212> PRT  
<213> Homo sapiens

<400> 101  
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Glu Lys Glu Gln Arg Trp Gly Ala Lys Thr Ile Glu Gly Ser Gly Arg  
35 40 45

Thr Glu His Ile Asn Ile His Gln Leu Arg Asn Lys Val Ser Glu Glu  
 50 55 60

His Asp Val Leu Arg Lys Lys Glu Met Glu Ser Gly Pro Lys Ala Ser  
 65 70 75 80

His Gly Tyr Gly Gly Arg Phe Gly Val Glu Arg Asp Arg Met Asp Lys  
 85 90 95

Ser Ala Val Gly His Glu Tyr Val Ala Glu Val Glu Lys His Ser Ser  
 100 105 110

Gln Thr Asp Ala Ala Lys Gly Phe Gly Gly Lys Tyr Gly Val Glu Arg  
 115 120 125

Asp Arg Ala Asp Lys Ser Ala Val Gly Phe Asp Tyr Lys Gly Glu Val  
 130 135 140

Glu Lys His Thr Ser Gln Lys Asp Tyr Ser Arg Gly Phe Gly Gly Arg  
 145 150 155 160

Tyr Gly Val Glu Lys Asp Lys Trp Asp Lys Ala Ala Leu Gly Tyr Asp  
 165 170 175

Tyr Lys Gly Glu Thr Glu Lys His Glu Ser Gln Arg Asp Tyr Ala Lys  
 180 185 190

Gly Phe Gly Gly Gln Tyr Gly Ile Gln Lys Asp Arg Val Asp Lys Ser  
 195 200 205

Ala Val Gly Phe Asn Glu Met Glu Ala Pro Thr Thr Ala Tyr Lys Lys  
 210 215 220

Thr Thr Pro Ile Glu Ala Ala Ser Ser Gly Ala Arg Gly Leu Lys Ala  
 225 230 235 240

Lys Phe Glu Ser Met Ala Glu Glu Lys Arg Lys Arg Glu Glu Glu  
 245 250 255

Lys Ala Gln Gln Val Ala Arg Arg Gln Gln Glu Arg Lys Ala Val Thr  
 260 265 270

Lys Arg Ser Pro Glu Ala Pro Gln Pro Val Ile Ala Met Glu Glu Pro  
 275 280 285

Ala Val Pro Ala Pro Leu Pro Lys Lys Ile Ser Ser Glu Ala Trp Pro  
 290 295 300

Pro Val Gly Thr Pro Pro Ser Ser Glu Ser Glu Pro Val Arg Thr Ser  
 305 310 315 320

Arg Glu His Pro Val Pro Leu Leu Pro Ile Arg Gln Thr Leu Pro Glu  
 325 330 335

Asp Asn Glu Glu Pro Pro Ala Leu Pro Pro Arg Thr Leu Glu Gly Leu  
 340 345 350

Gln Val Glu Glu Glu Pro Val Tyr Glu Ala Glu Pro Glu Pro Glu Pro  
 355 360 365

Glu Pro Glu Pro Glu Pro Glu Asn Asp Tyr Glu Asp Val Glu Glu Met  
370 375 380

Asp Arg His Glu Gln Glu Asp Glu Pro Glu Gly Asp Tyr Glu Glu Val  
385 390 395 400

Leu Glu Pro Glu Asp Ser Ser Phe Ser Ser Ala Leu Ala Gly Ser Ser  
405 410 415

Gly Cys Pro Ala Gly Ala Gly Ala Val Ala Leu Gly Ile Ser  
420 425 430

Ala Val Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser  
435 440 445

Phe Asp Pro Asp Asp Val Ile Thr Asp Ile Glu Met Val Asp Glu Gly  
450 455 460

Trp Trp Arg Gly Arg Cys His Gly His Phe Gly Leu Phe Pro Ala Asn  
465 470 475 480

Tyr Val Lys Leu Leu Glu  
485

<210> 102

<211> 96

<212> DNA

<213> Homo sapiens

<400> 102

ctgacagcat ctggctttca gttcctcagt caccactact ttgtacccaaa ttcactgttt 60  
tggtctgaa atctaatttt gagtttagca aggatg 96

<210> 103

<211> 349

<212> DNA

<213> Homo sapiens

<400> 103

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ccacggcaag gacatcccccc tcgaactcag gcagctcctt tttgcagcct ggctcgagtt 180  
ggctcagcac aaaaggtaaa aagatgcaga gaccccgagcc tcggatgaac ctcctctgcg 240  
ccaaacccgct gtccgatttg aatttcttca gcacgcgccc cctgactctc tccagcctct 300  
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<210> 104

<211> 116

<212> PRT

<213> Homo sapiens

<400> 104

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Gln Arg Leu Glu Arg Val Arg Gly Arg Val Leu Lys Lys Phe Lys Ser  
20 25 30

Asp Ser Gly Leu Ala Gln Arg Arg Phe Ile Arg Gly Trp Gly Leu Cys  
35 40 45

Ile Phe Leu Pro Phe Val Leu Ser Gln Leu Glu Pro Gly Cys Lys Lys  
50 55 60

Glu Leu Pro Glu Phe Glu Gly Asp Val Leu Ala Val Gly Ser Gln Ala  
65 70 75 80

Leu Thr Thr Glu Gly Ile Tyr Glu Asp Val Ile Arg Gly Cys Leu Leu  
85 90 95

Gln Arg Ile Asp Gln Glu Leu Lys Lys Thr Leu Gly Ala Asn Asp Val  
100 105 110

Ser Cys Thr Leu  
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<210> 105

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1)..(311)

<223> n = g, a, c or t

<400> 105

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gcttaggaaac aaacccaaaa ggctcacagc aagcggagaa aaaaacccca aaatctgtaa 180  
cctgtatcac aaagcgttca tatccttcag atataaagag ttatttagata tcaataagaa 240  
aaatgcaaac actcctgaaa agtagaaaaa agctatgaac aggcaattca ctgaaaattaa 300  
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<210> 106

<211> 5107

<212> DNA

<213> Homo sapiens

<400> 106

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gcacttc 5107

<210> 107  
<211> 579  
<212> PRT  
<213> Homo sapiens

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His Leu Arg Gly Gln Val Asp Thr Leu Leu Arg Asn Phe Leu Pro Cys  
35 40 45  
  
Tyr Arg Gly Gln Leu Ala Ala Ser Val Leu Arg Gln Ile Ser Arg Glu  
50 55 60  
  
Leu Gly Pro Gln Glu Pro Thr Gly Ser Gln Leu Leu Arg Ser Lys Lys  
65 70 75 80  
  
Leu Pro Arg Val Arg Glu His Arg Gly Pro Leu Thr Gln Leu Arg Gly  
85 90 95  
  
His Pro Pro Arg Trp Gln Pro Ile Phe Cys Val Leu Arg Gly Asp Gly  
100 105 110  
  
Arg Leu Glu Trp Phe Ser His Lys Glu Glu Tyr Glu Asn Gly Gly His  
115 120 125  
  
Cys Leu Gly Ser Thr Ala Leu Thr Gly Tyr Thr Leu Leu Thr Ser Gln  
130 135 140  
  
Arg Glu Tyr Leu Arg Leu Leu Asp Ala Leu Cys Pro Glu Ser Leu Gly  
145 150 155 160  
  
Asp His Thr Gln Glu Glu Pro Asp Ser Leu Leu Glu Val Pro Val Ser  
165 170 175  
  
Phe Pro Leu Phe Leu Gln His Pro Phe Arg Arg His Leu Cys Phe Ser  
180 185 190  
  
Ala Ala Thr Arg Glu Ala Gln His Ala Trp Arg Leu Ala Leu Gln Gly  
195 200 205  
  
Gly Ile Arg Leu Gln Gly Thr Val Leu Gln Arg Ser Gln Ala Pro Ala  
210 215 220  
  
Ala Arg Ala Phe Leu Asp Ala Val Arg Leu Tyr Arg Gln His Gln Gly  
225 230 235 240

His Phe Gly Asp Asp Asp Val Thr Leu Gly Ser Asp Ala Glu Val Leu  
 245 250 255

Thr Ala Val Leu Met Arg Glu Gln Leu Pro Ala Leu Arg Ala Gln Thr  
 260 265 270

Leu Pro Gly Leu Arg Gly Ala Gly Arg Ala Arg Ala Trp Ala Trp Thr  
 275 280 285

Glu Leu Leu Asp Ala Val His Ala Ala Val Leu Ala Gly Ala Ser Ala  
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Gly Leu Cys Ala Phe Gln Pro Glu Lys Asp Glu Leu Leu Ala Ser Leu  
 305 310 315 320

Glu Lys Thr Ile Arg Pro Asp Val Asp Gln Leu Leu Arg Gln Arg Ala  
 325 330 335

Arg Val Ala Gly Arg Leu Arg Thr Asp Ile Arg Gly Pro Leu Glu Ser  
 340 345 350

Cys Leu Arg Arg Glu Val Asp Pro Gln Leu Pro Arg Val Val Gln Thr  
 355 360 365

Leu Leu Arg Thr Val Glu Ala Ser Leu Glu Ala Val Arg Thr Leu Leu  
 370 375 380

Ala Gln Gly Met Asp Arg Leu Ser His Arg Leu Arg Gln Ser Pro Ser  
 385 390 395 400

Gly Thr Arg Leu Arg Arg Glu Val Tyr Ser Phe Gly Glu Met Pro Trp  
 405 410 415

Asp Leu Ala Leu Met Gln Thr Cys Tyr Arg Glu Ala Glu Arg Ser Arg  
 420 425 430

Gly Arg Leu Gly Gln Leu Ala Ala Pro Phe Gly Phe Leu Gly Met Gln  
 435 440 445

Ser Leu Val Phe Gly Ala Gln Asp Leu Ala Gln Gln Leu Met Ala Asp  
 450 455 460

Ala Val Ala Thr Phe Leu Gln Leu Ala Asp Gln Cys Léu Thr Thr Ala  
 465 470 475 480

Leu Asn Cys Asp Gln Ala Ala Gln Arg Leu Glu Arg Val Arg Gly Arg  
 485 490 495

Val Leu Lys Lys Phe Lys Ser Asp Ser Gly Leu Ala Gln Arg Arg Phe  
 500 505 510

Ile Arg Gly Trp Gly Leu Cys Ile Phe Leu Pro Phe Val Leu Ser Gln  
 515 520 525

Leu Glu Pro Gly Cys Lys Lys Thr Glu Ser Arg Ser Val Ala Gln Ala  
 530 535 540

Val Val Gln Trp Cys Asp Leu Gly Ser Leu Arg Pro Pro Pro Pro Arg  
 545 550 555 560

Phe Lys Arg Ser Ser His Leu Gly Leu Pro Ser Ser Trp Asp Tyr Arg  
565 570 575

His Pro Leu

<210> 108  
<211> 2917  
<212> DNA  
<213> Homo sapiens

<400> 108  
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cctgtggaaa caggagccac ctgctcagga gacccttgc ctgaggaagt ctttacctct 240  
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atggggcag ctgtcatggc tggcggcggc acttttctc agagtttctg ctttgcgtt 360  
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ggtcagatta aaacaaaaaaa ctgccaaaag catcccccttgc gccccccatg tggcactggc 480  
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taaggactcc acccctcaga gctcactcag accccaagga cagaggtgac tggggcttgg 600  
tgacttgttc actccctttt tcccaggtat actgaagggg tgacagagag aggtcttcat 660  
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gtcccttcag ctcagctgct cttctcccc accaccctg ggatgtgggt gctctgggt 840  
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<210> 109  
<211> 83  
<212> PRT  
<213> Homo sapiens

<400> 109  
Met Glu Ser Arg Ser Val Ala Gln Ala Gly Val Gln Trp Pro Asp Leu  
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Gly Ser Leu Gln Pro Leu Pro Pro Arg Phe Lys Arg Phe Phe Cys Leu  
20 25 30  
  
Ser Leu Gln Ser Ser Trp Asp Tyr Arg His Ala Pro Pro Arg Pro Ala  
35 40 45  
  
Asn Phe Val Phe Leu Val Glu Thr Gly Phe Cys His Val Ser Gln Ala  
50 55 60  
  
Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Pro Arg Pro Pro Lys  
65 70 75 80  
  
Val Leu Arg

<210> 110  
<211> 509  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (467)  
<223> n = g, a, c or t

<400> 110  
aaaccttaag aaccacataa tactatataa tgctttctg tacaaatctc aagaaacact 60  
ttcatttcatt aaaacatcat gaaaatcctt aaatgtgtta aatggaaaaa aatgaaacca 120  
tgaacaaaaa agctatacat gtaggtgcat atttatctcc tcctgagttg ggagaaatct 180  
ttcttaagcat agaaaacaatg gtagcaaaag agaagaatag atttggctgg attaacaata 240  
aaaaatttctt gccagaaaata tgaaaattca atttagacaa aattcaatat aaacaaaatt 300  
aatatagaca aaggtggtaa acaggtggtt ctcagagaag ataaatacat gattatcaa 360  
cataaaaaga aatgttcaat gtttctagaa gacaaataat tacaaaccta aacaaattgt 420  
atatttgtta gattggcata aattataata atccaacatt gagttangtg gaatataaaat 480  
tggtaaaata tttctggaag acaatttgg 509

<210> 111  
<211> 525  
<212> DNA  
<213> Homo sapiens

<400> 111  
agaagtgatt atgggattaa aagaatacat aattacagtg ttttgggatt gggcttttt 60  
ttttcttaat agaaaagcag aaacttcata aataatagct gtgcatttgc taccagataa 120  
caaatattgt ttcccctgaa gatatgacct actagaacta ctcacatata tagtccaata 180  
attgctgact taataggtat ggtaaaatag ctgataataa gtcagactct caagagttc 240  
tgtacattga ttattgacaa attcattgtt ttacatccta ctaaagaaca tgtgtgtggg 300  
gaggggggtgg ggaactggtt cacaacataa tctgaaggag atcaaacatc tctaaggaca 360  
ggtacccagt gatgataata tatctgaaaa cacaagccat ttttattctt tatcccaatt 420  
aacttgaggt actctaataatg tgaagcactc gattgcacta tgacccctt gagtgtatggg 480  
cagcttgggtt cctctctcac ttttggttc ttttaataat gcaaa 525

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<210> 112
<211> 183
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1)..(183)
<223> n = g, a, c or t

<400> 112
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cagtaacaac gtaggcttgg aggatggtn caatgaaaat gattctgtt cggaaacgtt 120
ttgactttgg actgtanaag cttttctttg atcacctgtg ntggaggaaa ggaaagaagc 180
ctt 183

<210> 113
<211> 1750
<212> DNA
<213> Homo sapiens

<400> 113
cagctctctg tcagaatggc caccatggta ccatccgtgt tggcccccag ggcctgtgg 60
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gtggagcccc agaaccctgt gctctctgtt ggagggtccc tggtttgtgaa ctgcagtact 180
gattgtccca gctctgagaa aatgcctt gagacgtccc tatcaaagga gttgggtggcc 240
agtggcatgg gctggcagc cttcaatctc agcaacgtga ctggcaacag tcggatcctc 300
tgctcagtgt actgcaatgg ctcccagata acaggctct ctaacatcac cgtgtacggg 360
ctcccgagc gtgtggagct ggcacccctg cttttgtggc agccgggtggg ccagaacttc 420
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atgcagcccc aggggctggg actgttcgtg aacacctcg ccccccggca gtcggaaacc 660
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acagaagcaa tggggaaaga accgtccaga gctgagtgac gctggatcc gggatcaaag 1680
ttggcgggggg cttggctgtt ccctcagatt ccgcaccaat aaagccttca aactccctaa 1740
aaaaaaaaaa 1750

<210> 114
<211> 547
<212> PRT
<213> Homo sapiens

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<400> 114  
 Met Ala Thr Met Val Pro Ser Val Leu Trp Pro Arg Ala Cys Trp Thr  
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 20 25 30  
  
 Leu Leu Arg Val Glu Pro Gln Asn Pro Val Leu Ser Ala Gly Gly Ser  
 35 40 45  
  
 Leu Phe Val Asn Cys Ser Thr Asp Cys Pro Ser Ser Glu Lys Ile Ala  
 50 55 60  
  
 Leu Glu Thr Ser Leu Ser Lys Glu Leu Val Ala Ser Gly Met Gly Trp  
 65 70 75 80  
  
 Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser Arg Ile Leu Cys  
 85 90 95  
  
 Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser Ser Asn Ile Thr  
 100 105 110  
  
 Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Pro Trp  
 115 120 125  
  
 Gln Pro Val Gly Gln Asn Phe Thr Leu Arg Cys Gln Val Glu Gly Gly  
 130 135 140  
  
 Ser Pro Arg Thr Ser Leu Thr Val Val Leu Leu Arg Trp Glu Glu Glu  
 145 150 155 160  
  
 Leu Ser Arg Gln Pro Ala Val Glu Glu Pro Ala Glu Val Thr Ala Thr  
 165 170 175  
  
 Val Leu Ala Ser Arg Asp Asp His Gly Ala Pro Phe Ser Cys Arg Thr  
 180 185 190  
  
 Glu Leu Asp Met Gln Pro Gln Gly Leu Gly Leu Phe Val Asn Thr Ser  
 195 200 205  
  
 Ala Pro Arg Gln Leu Arg Thr Phe Val Leu Pro Val Thr Pro Pro Arg  
 210 215 220  
  
 Leu Val Ala Pro Arg Phe Leu Glu Val Glu Thr Ser Trp Pro Val Asp  
 225 230 235 240  
  
 Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala Gln Val Tyr Leu  
 245 250 255  
  
 Ala Leu Gly Asp Gln Met Leu Asn Ala Thr Val Met Asn His Gly Asp  
 260 265 270  
  
 Thr Leu Thr Ala Thr Ala Thr Ala Arg Ala Asp Gln Glu Gly  
 275 280 285  
  
 Ala Arg Glu Ile Val Cys Asn Val Thr Leu Gly Gly Glu Arg Arg Glu  
 290 295 300  
  
 Ala Arg Glu Asn Leu Thr Val Phe Ser Phe Leu Gly Pro Ile Val Asn  
 305 310 315 320

Leu Ser Glu Pro Thr Ala His Glu Gly Ser Thr Val Thr Val Ser Cys  
 325 330 335  
 Met Ala Gly Ala Arg Val Gln Val Thr Leu Asp Gly Val Pro Ala Ala  
 340 345 350  
 Ala Pro Gly Gln Pro Ala Gln Leu Gln Leu Asn Ala Thr Glu Ser Asp  
 355 360 365  
 Asp Gly Arg Ser Phe Phe Cys Ser Ala Thr Leu Glu Val Asp Gly Glu  
 370 375 380  
 Phe Leu His Arg Asn Ser Ser Val Gln Leu Arg Val Leu Tyr Gly Pro  
 385 390 395 400  
 Lys Ile Asp Arg Ala Thr Cys Pro Gln His Leu Lys Trp Lys Asp Lys  
 405 410 415  
 Thr Arg His Val Leu Gln Cys Gln Ala Arg Gly Asn Pro Tyr Pro Glu  
 420 425 430  
 Leu Arg Cys Leu Lys Glu Gly Ser Ser Arg Glu Val Pro Val Gly Ile  
 435 440 445  
 Pro Phe Phe Val Asn Val Thr His Asn Gly Thr Tyr Gln Cys Gln Ala  
 450 455 460  
 Ser Ser Ser Arg Gly Lys Tyr Thr Leu Val Val Val Met Asp Ile Glu  
 465 470 475 480  
 Ala Gly Ser Ser His Phe Val Pro Val Phe Val Ala Val Leu Leu Thr  
 485 490 495  
 Leu Gly Val Val Thr Ile Val Leu Ala Leu Met Tyr Val Phe Arg Glu  
 500 505 510  
 His Gln Arg Ser Gly Ser Tyr His Val Arg Glu Glu Ser Thr Tyr Leu  
 515 520 525  
 Pro Leu Thr Ser Met Gln Pro Thr Glu Ala Met Gly Glu Glu Pro Ser  
 530 535 540  
 Arg Ala Glu  
 545

<210> 115  
 <211> 275  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
 cctgatgccc gaatttcagt ttggcactta cagcgaatct gagagaaaaa ccgaggagta 60  
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 tgtctattca ctcctgaata tcaaataaa gagctggtaac tcctggtaa tcaacagctt 180  
 cgtcaacggg gtctatgcct ttggtttctt cttcatgctg ccccgactct ttgtgaacta 240  
 caagttgaag tcagtggcac atctgccctg gaagg 275

<210> 116  
 <211> 2040  
 <212> DNA  
 <213> Homo sapiens

<400> 116

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ggcatgtac ggcacatcgatc acacccggcc gtgtccggc gacgcacact gcatccagcc 120
ctacctggcg cggcgccca agctgcagct gagcgtgtac accacgacga ggtcccacct 180
gggtgcttag aacaacatcg acctggctt gaatgtggaa gacttgcgtg tggagtccaa 240
atttggaaagg acagttaatg tttctgtacc aaagaaaaacg agaaaacaatg ggacgctgt 300
tgcctacatc ttccctccatc acgctgggt cctgcccgtgg cacgacggga agcaggtgca 360
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cggggagtct gatacacagc agatcgaggc ggagaagaag ccgacgagtg ccctggatga 480
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<210> 117  
 <211> 538  
 <212> PRT  
 <213> Homo sapiens

<400> 117

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Met Trp Ser Gly Arg Ser Ser Phe Thr Ser Leu Val Val Gly Val Phe
1 5 10 15
  
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```

Val Val Tyr Val Val His Thr Cys Trp Val Met Tyr Gly Ile Val Tyr
20 25 30
  
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```

Thr Arg Pro Cys Ser Gly Asp Ala Asn Cys Ile Gln Pro Tyr Leu Ala
35 40 45
  
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Arg Arg Pro Lys Leu Gln Leu Ser Val Tyr Thr Thr Arg Ser His
50 55 60
  
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Leu Gly Ala Glu Asn Asn Ile Asp Leu Val Leu Asn Val Glu Asp Phe  
 65 70 75 80

Asp Val Glu Ser Lys Phe Glu Arg Thr Val Asn Val Ser Val Pro Lys  
 85 90 95

Lys Thr Arg Asn Asn Gly Thr Leu Tyr Ala Tyr Ile Phe Leu His His  
 100 105 110

Ala Gly Val Leu Pro Trp His Asp Gly Lys Gln Val His Leu Val Ser  
 115 120 125

Pro Leu Thr Thr Tyr Met Val Pro Lys Pro Glu Glu Ile Asn Leu Leu  
 130 135 140

Thr Gly Glu Ser Asp Thr Gln Gln Ile Glu Ala Glu Lys Lys Pro Thr  
 145 150 155 160

Ser Ala Leu Asp Glu Pro Val Ser His Trp Arg Pro Arg Leu Ala Leu  
 165 170 175

Asn Val Met Ala Asp Asn Phe Val Phe Asp Gly Ser Ser Leu Pro Ala  
 180 185 190

Asp Val His Arg Tyr Met Lys Met Ile Gln Leu Gly Lys Thr Val His  
 195 200 205

Tyr Leu Pro Ile Leu Phe Ile Asp Gln Leu Ser Asn Arg Val Lys Asp  
 210 215 220

Leu Met Val Ile Asn Arg Ser Thr Thr Glu Leu Pro Leu Thr Val Ser  
 225 230 235 240

Tyr Asp Lys Val Ser Leu Gly Arg Leu Arg Phe Trp Ile His Met Gln  
 245 250 255

Asp Ala Val Tyr Ser Leu Gln Gln Phe Gly Phe Ser Glu Lys Asp Ala  
 260 265 270

Asp Glu Val Lys Gly Ile Phe Val Asp Thr Asn Leu Tyr Phe Leu Ala  
 275 280 285

Leu Thr Phe Phe Val Ala Ala Phe His Leu Leu Phe Asp Phe Leu Ala  
 290 295 300

Phe Lys Asn Asp Ile Ser Phe Trp Lys Lys Lys Ser Met Ile Gly  
 305 310 315 320

Met Ser Thr Lys Ala Val Leu Trp Arg Cys Phe Ser Thr Val Val Ile  
 325 330 335

Phe Leu Phe Leu Leu Asp Glu Gln Thr Ser Leu Leu Val Leu Val Pro  
 340 345 350

Ala Gly Val Gly Ala Ala Ile Glu Leu Trp Lys Val Lys Lys Ala Leu  
 355 360 365

Lys Met Thr Ile Phe Trp Arg Gly Leu Met Pro Glu Phe Gln Phe Gly  
 370 375 380

Thr Tyr Ser Glu Ser Glu Arg Lys Thr Glu Glu Tyr Asp Thr Gln Ala  
 385 390 395 400  
 Met Lys Tyr Leu Ser Tyr Leu Leu Tyr Pro Leu Cys Val Gly Gly Ala  
 405 410 415  
 Val Tyr Ser Leu Leu Asn Ile Lys Tyr Lys Ser Trp Tyr Ser Trp Leu  
 420 425 430  
 Ile Asn Ser Phe Val Asn Gly Val Tyr Ala Phe Gly Phe Leu Phe Met  
 435 440 445  
 Leu Pro Gln Leu Phe Val Asn Tyr Lys Leu Lys Ser Val Ala His Leu  
 450 455 460  
 Pro Trp Lys Ala Phe Thr Tyr Lys Ala Phe Asn Thr Phe Ile Asp Asp  
 465 470 475 480  
 Val Phe Ala Phe Ile Ile Thr Met Pro Thr Ser His Arg Leu Ala Cys  
 485 490 495  
 Phe Arg Asp Asp Val Val Phe Leu Val Tyr Leu Tyr Gln Arg Trp Leu  
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 Tyr Pro Val Asp Lys Arg Arg Val Asn Glu Phe Gly Glu Ser Tyr Glu  
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 ctccccgatc attacattgg tggcccttga tgaagccctt gacaactaca ccatcacatt 240  
 cctcatccgc ggtgtggcca tcggccagac cagtcataact gcaagtgtga ccaataaagc 300  
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 ccagcctcag tccaaatcc tttctccat cagaatgag agcgttgcgc tggtagcgc 480  
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 catcattgtt gctgtaaagg tatccctgtt ttcctacatg agggtttcca tgagccctgt 1260  
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 35 40 45

Tyr Phe Pro Phe Met Asp Leu Lys Leu Arg Ala Ala Ser Pro Ile Ile  
 50 55 60

Thr Leu Val Ala Leu Asp Glu Ala Leu Asp Asn Tyr Thr Ile Thr Phe  
 65 70 75 80

Leu Ile Arg Gly Val Ala Ile Gly Gln Thr Ser Leu Thr Ala Ser Val  
 85 90 95

Thr Asn Lys Ala Gly Gln Arg Ile Asn Ser Ala Pro Gln Gln Ile Glu  
 100 105 110

Val Phe Pro Pro Phe Arg Leu Met Pro Arg Lys Val Thr Leu Leu Ile  
 115 120 125

Gly Ala Thr Met Gln Val Thr Ser Glu Gly Gly Pro Gln Pro Gln Ser  
 130 135 140

Asn Ile Leu Phe Ser Ile Ser Asn Glu Ser Val Ala Leu Val Ser Ala  
 145 150 155 160

Ala Gly Leu Val Gln Gly Leu Ala Ile Gly Asn Gly Thr Val Ser Gly  
 165 170 175

Leu Val Gln Ala Val Asp Ala Glu Thr Gly Lys Val Val Ile Ile Ser  
 180 185 190

Gln Asp Leu Val Gln Val Glu Val Leu Leu Leu Arg Ala Val Arg Ile  
 195 200 205

Arg Ala Pro Ile Met Arg Met Arg Thr Gly Thr Gln Met Pro Ile Tyr  
 210 215 220

Val Thr Gly Ile Thr Asn His Gln Asn Pro Phe Ser Phe Gly Asn Ala  
 225 230 235 240

Val Pro Gly Leu Thr Phe His Trp Ser Val Thr Lys Arg Asp Val Leu  
 245 250 255

Asp Leu Arg Gly Arg His His Glu Ala Ser Ile Arg Leu Pro Ser Gln  
 260 265 270

Tyr Asn Phe Ala Met Asn Val Leu Gly Arg Val Lys Gly Arg Thr Gly  
 275 280 285

Leu Arg Val Val Val Lys Ala Val Asp Pro Thr Ser Gly Gln Leu Tyr  
 290 295 300

Gly Leu Ala Arg Glu Leu Ser Asp Glu Ile Gln Val Gln Val Phe Glu  
 305 310 315 320

Lys Leu Gln Leu Leu Asn Pro Glu Ile Glu Ala Glu Gln Ile Leu Met  
 325 330 335

Ser Pro Asn Ser Tyr Ile Lys Leu Gln Thr Asn Arg Asp Gly Ala Ala  
 340 345 350

Ser Leu Ser Tyr Arg Val Leu Asp Gly Pro Glu Lys Val Pro Val Val  
 355 360 365  
 His Val Asp Glu Lys Gly Phe Leu Ala Ser Gly Ser Met Ile Gly Thr  
 370 375 380  
 Ser Thr Ile Glu Val Ile Ala Gln Glu Pro Phe Gly Ala Asn Gln Thr  
 385 390 395 400  
 Ile Ile Val Ala Val Lys Val Ser Pro Val Ser Tyr Leu Arg Val Ser  
 405 410 415  
 Met Ser Pro Val Leu His Thr Gln Asn Lys Glu Ala Leu Val Ala Val  
 420 425 430  
 Pro Leu Gly Met Thr Val Thr Phe Thr Val His Phe His Asp Asn Ser  
 435 440 445  
 Gly Asp Val Phe His Ala His Ser Ser Val Leu Asn Phe Ala Thr Asn  
 450 455 460  
 Arg Asp Asp Phe Val Gln Ile Gly Lys Gly Pro Thr Asn Asn Thr Cys  
 465 470 475 480  
 Val Val Arg Thr Val Ser Val Gly Leu Thr Leu Leu Arg Val Trp Asp  
 485 490 495  
 Ala Glu His Pro Gly Leu Ser Asp Phe Met Pro Leu Pro Val Leu Gln  
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 Ala Ile Ser Pro Glu Leu Ser Gly Ala Met Val Val Gly Asp Val Leu  
 515 520 525  
 Cys Leu Ala Thr Val Leu Thr Ser Leu Glu Gly Leu Ser Gly Thr Trp  
 530 535 540  
 Ser Ser Ser Ala Asn Ser Ile Leu His Ile Asp Pro Lys Thr Gly Val  
 545 550 555 560  
 Ala Val Ala Arg Ala Val Gly Ser Val Thr Val Tyr Tyr Glu Val Ala  
 565 570 575  
 Gly His Leu Arg Thr Tyr Lys Glu Val Val Val Ser Val Pro Gln Arg  
 580 585 590  
 Ile Met Ala Arg His Leu His Pro Ile Gln Thr Ser Phe Gln Glu Ala  
 595 600 605  
 Thr Ala Ser Lys Val Ile Val Ala Val Gly Asp Arg Ser Ser Asn Leu  
 610 615 620  
 Arg Gly Glu Cys Thr Pro Thr Gln Arg Glu Val Ile Gln Ala Leu His  
 625 630 635 640  
 Pro Glu Thr Leu Ile Ser Cys Gln Ser Gln Phe Lys Pro Ala Val Phe  
 645 650 655  
 Asp Phe Pro Ser Gln Asp Val Phe Thr Val Glu Pro Gln Phe Asp Thr  
 660 665 670  
 Ala Leu Gly Gln Tyr Phe Cys Ser Ile Thr Met His Arg Leu Thr Asp

675	680	685
Lys Gln Arg Lys His Leu Ser Met Lys Lys Thr Ala Leu Val Val Ser		
690	695	700
Ala Ser Leu Ser Ser Ser His Phe Ser Thr Glu Gln Val Gly Ala Glu		
705	710	715
Val Pro Phe Ser Pro Gly Leu Phe Ala Asp Gln Ala Glu Ile Leu Leu		
725	730	735
Ser Asn His Tyr Thr Ser Ser Glu Ile Arg Val Phe Gly Ala Pro Glu		
740	745	750
Val Leu Glu Asn Leu Glu Val Lys Ser Gly Ser Pro Ala Val Leu Ala		
755	760	765
Phe Ala Lys Glu Lys Ser Phe Gly Trp Pro Ser Phe Ile Thr Tyr Thr		
770	775	780
Val Gly Val Ser Asp Pro Ala Ala Gly Ser Gln Gly Pro Leu Ser Thr		
785	790	795
Thr Leu Thr Phe Ser Ser Pro Val Thr Asn Gln Ala Ile Ala Ile Pro		
805	810	815
Val Thr Val Ala Phe Val Met Asp Arg Arg Gly Pro Gly Pro Tyr Gly		
820	825	830
Ala Ser Leu Phe Gln His Phe Leu Asp Ser Tyr Gln Val Met Phe Phe		
835	840	845
Thr Leu Phe Ala Leu Leu Ala Gly Thr Ala Val Met Ile Ile Ala Tyr		
850	855	860
His Thr Val Cys Thr Pro Arg Asp Leu Ala Val Pro Ala Ala Leu Thr		
865	870	875
Pro Arg Ala Ser Pro Gly His Ser Pro His Tyr Phe Ala Ala Ser Ser		
885	890	895
Pro Thr Ser Pro Asn Ala Leu Pro Pro Ala Arg Lys Ala Ser Pro Pro		
900	905	910
Ser Gly Leu Trp Ser Pro Ala Tyr Ala Ser His		
915	920	
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                  35                 40                 45  
  
 Cys Phe Thr Gln Lys Leu Val Glu Lys Leu Tyr Ser Gly Met Phe Ser  
                  50                 55                 60  
  
 Ala Asp Pro Arg His Ile Leu Leu Phe Ile Leu Glu His Ile Met Val  
                  65                 70                 75                 80  
  
 Val Ile Glu Thr Ala Ser Ser Gln Arg Asp Thr Val Leu Ser Thr Leu  
                  85                 90                 95  
  
 Tyr Ser Ser Leu Asn Lys Val Ile Leu Tyr Cys Leu Ser Lys Pro Gln  
                  100                 105                 110  
  
 Gln Ser Leu Ser Glu Cys Leu Gly Leu Leu Ser Ile Leu Gly Phe Leu  
                  115                 120                 125  
  
 Gln Glu His Trp Asp Val Val Phe Ala Thr Tyr Asn Ser Asn Ile Ser  
                  130                 135                 140  
  
 Phe Leu Leu Cys Leu Met His Cys Leu Leu Leu Leu Asn Glu Arg Ser  
                  145                 150                 155                 160  
  
 Tyr Pro Glu Gly Phe Gly Leu Glu Pro Lys Pro Arg Met Ser Thr Tyr  
                  165                 170                 175  
  
 His Gln Val Phe Leu Ser Pro Asn Glu Asp Val Lys Glu Lys Arg Glu  
                  180                 185                 190  
  
 Asp Leu Pro Ser Leu Ser Asp Val Gln His Asn Ile Gln Lys Thr Val  
                  195                 200                 205  
  
 Gln Thr Leu Trp Gln Gln Leu Val Ala Gln Arg Gln Gln Thr Leu Glu  
                  210                 215                 220  
  
 Asp Ala Phe Lys Ile Asp Leu Ser Val Lys Pro Gly Glu Arg Glu Val  
                  225                 230                 235                 240  
  
 Lys Ile Glu Glu Val Thr Pro Leu Trp Glu Glu Thr Met Leu Lys Ala  
                  245                 250                 255  
  
 Trp Gln His Tyr Leu Ala Ser Glu Lys Lys Ser Leu Ala Ser Arg Ser  
                  260                 265                 270  
  
 Asn Val Ala His His Ser Lys Val Thr Leu Trp Ser Gly Ser Leu Ser  
                  275                 280                 285  
  
 Ser Ala Met Lys Leu Met Pro Gly Arg Gln Ala Lys Asp Pro Glu Cys  
                  290                 295                 300  
  
 Lys Thr Glu Asp Phe Val Ser Cys Ile Glu Asn Tyr Arg Arg Arg Gly  
                  305                 310                 315                 320  
  
 Gln Glu Leu Tyr Ala Ser Leu Tyr Lys Asp His Val Gln Arg Arg Lys  
                  325                 330                 335  
  
 Cys Gly Asn Ile Lys Ala Ala Asn Ala Trp Ala Arg Ile Gln Glu Gln  
                  340                 345                 350

Leu Phe Gly Glu Leu Gly Leu Trp Ser Gln Gly Glu Glu Thr Lys Pro  
 355 360 365  
 Cys Ser Pro Trp Glu Leu Asp Trp Arg Glu Gly Pro Ala Arg Met Arg  
 370 375 380  
 Lys Arg Ile Lys Arg Leu Ser Pro Leu Glu Ala Leu Ser Ser Gly Arg  
 385 390 395 400  
 His Lys Glu Ser Gln Asp Lys Asn Asp His Ile Ser Gln Thr Asn Ala  
 405 410 415  
 Glu Asn Gln Asp Glu Leu Thr Leu Arg Glu Ala Glu Gly Glu Pro Asp  
 420 425 430  
 Glu Val Gly Val Asp Cys Thr Gln Leu Thr Phe Phe Pro Ala Leu His  
 435 440 445  
 Glu Ser Leu His Ser Glu Asp Phe Leu Glu Leu Cys Arg Glu Arg Gln  
 450 455 460  
 Val Ile Leu Gln Glu Leu Leu Asp Lys Glu Lys Val Thr Gln Lys Phe  
 465 470 475 480  
 Ser Leu Val Ile Val Gln Gly His Leu Val Ser Glu Gly Val Leu Leu  
 485 490 495  
 Phe Gly His Gln His Phe Tyr Ile Cys Glu Asn Phe Thr Leu Ser Pro  
 500 505 510  
 Thr Gly Asp Val Tyr Cys Thr Arg His Cys Leu Ser Asn Ile Ser Asp  
 515 520 525  
 Pro Phe Ile Phe Asn Leu Cys Ser Lys Asp Arg Ser Thr Asp His Tyr  
 530 535 540  
 Ser Cys Gln Cys His Ser Tyr Ala Asp Met Arg Glu Leu Arg Gln Ala  
 545 550 555 560  
 Arg Phe Leu Leu Gln Asp Ile Ala Leu Glu Ile Phe Phe His Asn Gly  
 565 570 575  
 Tyr Ser Lys Phe Leu Val Phe Tyr Asn Asn Asp Arg Ser Lys Ala Phe  
 580 585 590  
 Lys Ser Phe Cys Ser Phe Gln Pro Ser Leu Lys Gly Lys Ala Thr Ser  
 595 600 605  
 Glu Asp Thr Leu Asn Leu Arg Arg Tyr Pro Gly Ser Asp Arg Ile Met  
 610 615 620  
 Leu Gln Lys Trp Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu Met  
 625 630 635 640  
 Tyr Leu Asn Thr Ala Ala Gly Arg Thr Cys Asn Asp Tyr Met Gln Tyr  
 645 650 655  
 Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu Asn  
 660 665 670

Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly Ala  
 675 680 685  
 Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu Val  
 690 695 700  
 Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr His  
 705 710 715 720  
 Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro Pro  
 725 730 735  
 Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val Ala  
 740 745 750  
 Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser Arg  
 755 760 765  
 Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr Leu  
 770 775 780  
 Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met Gln  
 785 790 795 800  
 Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp Gly  
 805 810 815  
 Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser Asp  
 820 825 830  
 Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly Tyr  
 835 840 845  
 Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His Pro  
 850 855 860  
 Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro Leu  
 865 870 875 880  
 Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val Pro  
 885 890 895  
 Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly Lys  
 900 905 910  
 Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly His  
 915 920 925  
 Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln Val  
 930 935 940  
 Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro Lys  
 945 950 955 960  
 Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala Val  
 965 970 975  
 Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe Ser  
 980 985 990

Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser Asp  
 995 1000 1005  
 Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys Leu  
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 Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr Ser  
 1025 1030 1035 1040  
 Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro Arg  
 1045 1050 1055  
 Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val Thr  
 1060 1065 1070  
 Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser Gln  
 1075 1080 1085  
 Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val Thr  
 1090 1095 1100  
 Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser Asp  
 1105 1110 1115 1120  
 Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu Trp  
 1125 1130 1135  
 Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly Pro  
 1140 1145 1150  
 Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp Asp  
 1155 1160 1165  
 Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg Val  
 1170 1175 1180  
 Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala Gly  
 1185 1190 1195 1200  
 Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp Glu  
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 Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu Thr  
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 Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val Ser  
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 Cys Trp Ser Ala Asp Gly  
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<400> 121  
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 Tyr Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu  
 35 40 45  
 Asn Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly  
 50 55 60  
 Ala Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu  
 65 70 75 80  
 Val Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr  
 85 90 95  
 His Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro  
 100 105 110  
 Pro Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Ser Phe Asp Val  
 115 120 125  
 Ala Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser  
 130 135 140  
 Arg Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr  
 145 150 155 160  
 Leu Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met  
 165 170 175  
 Gln Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp  
 180 185 190  
 Gly Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser  
 195 200 205  
 Asp Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly  
 210 215 220  
 Tyr Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His  
 225 230 235 240  
 Pro Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro  
 245 250 255  
 Leu Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val  
 260 265 270  
 Pro Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly  
 275 280 285  
 Lys Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly  
 290 295 300  
 His Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln  
 305 310 315 320

Val Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro  
325 330 335

Lys Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala  
340 345 350

Val Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe  
355 360 365

Ser Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser  
370 375 380

Asp Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys  
385 390 395 400

Leu Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr  
405 410 415

Ser Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro  
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Arg Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val  
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Thr Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser  
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Gln Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val  
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Thr Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser  
485 490 495

Asp Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu  
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Trp Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly  
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Pro Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp  
530 535 540

Asp Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg  
545 550 555 560

Val Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala  
565 570 575

Gly Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp  
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Glu Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu  
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Thr Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val  
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Ser Arg Asn His Thr Lys Leu Leu Val Gly Asp Glu Arg Gly Arg Ile  
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Phe Cys Trp Ser Ala Asp Gly  
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